

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 258..422
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq XXLIIIINVGQLLA/QT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

```

AACCCACGGT GGGGGGAGCG CGGCCATGGC GCTCCTGCTT TCGGTGCTGC GTGTACTGCT    60
GGGCGGCTTC TTCGCGCTCG TGGGGTTGGC CAAGCTCTCG GAGGAGATCT CGGCTCCAGT    120
TTCGGAGCGG RTGRAATGCC CTGTTCGTGC AGTTTGCTGA TGTGTTCCCG CTGAAGGTAT    180
TTGGCTACCA GCCAGATCCC CTGAACTACC AAATAGCTGT GGGCTTTCTG GAACTGCTGG    240
CTGGGTTGCT GCTGGTC ATG GGC CCA CCG ATG CTG CAA GAG ATC AGT AAC    290
          Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn
          -55                -50                -45

TTG TTC TTG ATT CTG CTC ATG ATG GGG GCT ATC TTC ACC TTG GCA GCT    338
Leu Phe Leu Ile Leu Leu Met Met Gly Ala Ile Phe Thr Leu Ala Ala
          -40                -35                -30

CTG AAA GAG TCA CTA AGC ACC TGT ATC CCA GCC ATT GTC TGC CTG NGG    386
Leu Lys Glu Ser Leu Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Xaa
          -25                -20                -15

TDN CTG CTG CTG CTG AAT GTC GGC CAG CTC TTA GCC CAG ACT AAG AAG    434
Xaa Leu Leu Leu Leu Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys
          -10                -5                1

GTG GTC AGA CCC ACT AGG AAG AAG ACT CTA AGT ACA    470
Val Val Arg Pro Thr Arg Lys Lys Thr Leu Ser Thr
  5                10                15

```

## (2) INFORMATION FOR SEQ ID NO: 213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 4..55
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 19..70

id T18977  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 141..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 157..211  
id T18977  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 92..137  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 109..154  
id T18977  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 245..355  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..111  
id HSC12A111  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 321..355  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..35  
id W73324  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 133..345  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.6  
seq VVXFLLLLLAXLIA/TY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

```
AAGCAGCTTC CAGGATCCTG AGATCCGGAG CAGCCGGGGT CGGAGCGGCT CCTCAAGAGT   60
TACTGATCTA TNNATGGCAG AGAAAAAAAA ATTGTGACCA GAGACGTGTA GCAATGAACA   120
AGGAACRTCA TA ATG RWN NNK TTC ACA GAC CCC TCT TCA GTG AAT GAA AAG   171
      Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys
          -70                      -65                      -60

AAG AGG AGG GAG CGG GAA GAA AGG CAG AAT ATT GTC CTG TGG AGA CAG   219
Lys Arg Arg Glu Arg Glu Arg Gln Asn Ile Val Leu Trp Arg Gln
      -55                      -50                      -45
```

|   |     |
|---|-----|
| CCG CTC ATT ACC TTG CAG TAT TTT TCT CTG GAA ATC CTT GTA ATC TTG | 267 |
| Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu |     |
| -40 -35 -30   |     |
|   |     |
| AAG GAA TGG ACC TCA AAA TTA TGG CAT CGT CAM MGC ATT GTG GTG WCT | 315 |
| Lys Glu Trp Thr Ser Lys Leu Trp His Arg Xaa Xaa Ile Val Val Xaa |     |
| -25 -20 -15   |     |
|   |     |
| TTT TTA CTG CTG CTT GCT DGG CTT ATA GCT ACG TAT TAT             | 354 |
| Phe Leu Leu Leu Leu Ala Xaa Leu Ile Ala Thr Tyr Tyr             |     |
| -10 -5 1  |     |

## (2) INFORMATION FOR SEQ ID NO: 214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 189..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 75..197  
id AA021160  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 249..293
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6  
seq LLRGLLWXQVLCA/GP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

|   |     |
|---|-----|
| ACCTTTCTGG GTTGAGCATG GCTGAAGTGA CTCAGCCCAT GGGAGGTTTC CTAGGAGNAA | 60  |
| CAGGCTCCAC TTGCTGCCTC TCTGCGTGAA CTCCGTGTGC CGGCAACCTG GCGACCAGAC | 120 |
| TCCTGCCTTC GGAGGGGCTG GGGCTCCAGG ACCTGAGTGC CCCCCRNKGT TGGAAGGCGG | 180 |
| TGTCATATGT GCACAGAAGC CAAAAGCAT TGCTGGTATT TCGAAGGACT CTATCCAACC  | 240 |
| YHTTATAT ATG CCG CTC CTA CGA GGA CTG CTG TGG STC CAG GTG CTG TGT  | 290 |
| Met Pro Leu Leu Arg Gly Leu Leu Trp Xaa Gln Val Leu Cys           |     |
| -15 -10 -5  |     |
|   |     |
| GCG GGC CCT CTC CAT ACA GAG                                       | 311 |
| Ala Gly Pro Leu His Thr Glu                                       |     |

1

5

## (2) INFORMATION FOR SEQ ID NO: 215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 31..265  
id T78247  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 6..240  
id W17118  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 11..245  
id N88433  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..336
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 32..247  
id R35014  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 9..217  
id AA074562



est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 159..218
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.4  
seq AVVGCLLVPPAEA/NK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

```

AAGAGGCGGA GATGGCGGAG GGCGGTGGGA CGTGATGCGC GGGTCAGAGC CGGGCCTTGA      60
GAAGGAACTG GAGGCCCTTG GCAGCGGTGT CCCCTCGAGG ACCCCTCTGC CGGGCTCACC    120
AGGTGTCCGG CTTTGCTGGC CCAGCAAGCC TGATAAGC ATG AAG CTC TTA TCT TTG      176
                               Met Lys Leu Leu Ser Leu
                               -20                               -15

GTG GCT GTG GTC GGG TGT TTG CTG GTG CCC CCA GCT GAA GCC AAC AAG      224
Val Ala Val Val Gly Cys Leu Leu Val Pro Pro Ala Glu Ala Asn Lys
                -10                        -5                                1

AGT TCT GAA GAT ATC CRG TGC AAA TGC ATC TGT CCA CCT TAT AGA AAC      272
Ser Ser Glu Asp Ile Xaa Cys Lys Cys Ile Cys Pro Pro Tyr Arg Asn
                5                        10                        15

ATC AGT GGG CAC ATT TAC AAC CAG AAT GTA TCC CAG AAG GAC TGC AAC      320
Ile Ser Gly His Ile Tyr Asn Gln Asn Val Ser Gln Lys Asp Cys Asn
                20                        25                        30

TGC CTG CAC GTG GTG GAG CCC ATG CCA GTG CCG                          353
Cys Leu His Val Val Glu Pro Met Pro Val Pro
                35                        40                        45

```

## (2) INFORMATION FOR SEQ ID NO: 216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 15..332  
id HUM085F04B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 139..249
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 187..297  
id H85714  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 249..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 298..368  
id H85714  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..148
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 133..195  
id H85714  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 80..264  
id R77008  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 94..327  
id H49758  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 53..237  
id AA056366  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 114..185
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

```

AATTGGCTGG CTCTGGAGGC GCAGGTGGTC CTTCTTCTAC TGTCACATGG TGC GCGCTGT      60
TTTCTAATCA CGKGGCTGCC ACCCAGGCCT CTCTGCTCCT GTCKTKTGTT TGG ATG      116
                                     Met
CCG GCG CTG CTG CCT GTG GCC TCC CGC CTT TTG TTG CTA CCC CGA GTC      164
Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val
          -20                      -15                      -10
TTG CTG ACC ATG GCC TCT GGA AGC CCT CCG ACC CAG CCC TCG CCG GCC      212
Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala
          -5                      1                      5
TCG GAT TCC GGC TCT GGC TAC GTT CCG GGC TCG GTC TCT GCA GCC TTT      260
Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val Ser Ala Ala Phe
  10                      15                      20                      25
GTT ACT TGC CCC AAC GAG AAG GTC GCC AAG GAG ATC GCC AGG GCC GTK      308
Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile Ala Arg Ala Val
          30                      35                      40
GGG GAG AAG CGG      320
Gly Glu Lys Arg
          45

```

## (2) INFORMATION FOR SEQ ID NO: 217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..381
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 73..333  
id H95186  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..133
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 25..86  
id H95186  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 28..351
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLGLLSAEQLAEA/SV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

```

ACGGGTGCCG GGTGGAGCGA ASACGGA ATG TGT CTC CTG CTG GGG GCC ACG GGC      54
                        Met Cys Leu Leu Leu Gly Ala Thr Gly
                                -105                                -100

GTC GGG AAG ACG CTG CTG GTG AAA CGG CTG CAG GAG GTG AGC TCC CGG      102
Val Gly Lys Thr Leu Leu Val Lys Arg Leu Gln Glu Val Ser Ser Arg
                        -95                                -90                                -85

GAT GGG AAA GGC GAC CTG GGG GAG CCG CCC CCG ACA CGG CCC ACG GTG      150
Asp Gly Lys Gly Asp Leu Gly Glu Pro Pro Pro Thr Arg Pro Thr Val
                        -80                                -75                                -70

GGC ACC AAT CTT ACT GAC ATC GTG GCA CAG AGA AAG ATC ACC ATC CGG      198
Gly Thr Asn Leu Thr Asp Ile Val Ala Gln Arg Lys Ile Thr Ile Arg
                        -65                                -60                                -55

GAG CTT GGG GGG TGC ATG GGC CCC ATC TGG TCC AGT TAC TAT GGA AAC      246
Glu Leu Gly Gly Cys Met Gly Pro Ile Trp Ser Ser Tyr Tyr Gly Asn
                        -50                                -45                                -40

TGC CGT TCT CTC CTG TTT GTG ATG GAC GCC TCT GAC CCC ACC CAG CTC      294
Cys Arg Ser Leu Leu Phe Val Met Asp Ala Ser Asp Pro Thr Gln Leu
                        -35                                -30                                -25                                -20

TCT GCA TTM SGT GTG CAG CTC TTA GGT CTC CTT TCT GCA GAA CAA CTT      342
Ser Ala Xaa Xaa Val Gln Leu Leu Gly Leu Leu Ser Ala Glu Gln Leu
                        -15                                -10                                -5

GCA GAA GCA TCG GTG CTG ATA CTC TTC AAT AAA ATC GAC AAC      384
Ala Glu Ala Ser Val Leu Ile Leu Phe Asn Lys Ile Asp Asn
                        1                                5                                10

```

## (2) INFORMATION FOR SEQ ID NO: 218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 94..197  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 92..195  
id T93931  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..45  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..44  
id T93931  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 53..97  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 52..96  
id T93931  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 190..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 187..231  
id T93931  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 138..196  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 241..299  
id N25481  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 190..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 292..336  
id N25481  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 94..211  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 65..182  
id W19370  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 94..196
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 56..158  
id N35539  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 190..234
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 151..195  
id N35539  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 56..97
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 19..60  
id N35539  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 94..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 96..195  
id W87436  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..49
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 7..54  
id W87436  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 75..197
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7  
seq LLCLGQLHHPGLG/RV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

```
AAAGTTTGTT CCCCAGATTC GGAGCCTAGG AGCCCCCGCG GGCTGCGGCG CAGGTGCCCT    60
CGGCCTTAGT CGGG ATG GAG CTG CCT GCK GTG AAC CTT GAA AGT GAT TCT    110
      Met Glu Leu Pro Ala Val Asn Leu Glu Ser Asp Ser
        -40                      -35                      -30
```

|   |     |
|---|-----|
| CCT AGG TCA CTG GCT GCT GAC AAC CTG GGG CTG CAT TGT ATT CTC AGG | 158 |
| Pro Arg Ser Leu Ala Ala Asp Asn Leu Gly Leu His Cys Ile Leu Arg |     |
| -25 -20 -15   |     |
|   |     |
| CTC CTA TGC CTG GGC CAA CTT CAC CAT CCT GGC CTT GGG CGT GTG GGC | 206 |
| Leu Leu Cys Leu Gly Gln Leu His His Pro Gly Leu Gly Arg Val Gly |     |
| -10 -5 1  |     |
|   |     |
| TGT GGC TCA GCG GGA CTC CAT CGA CGC CGG                         | 236 |
| Cys Gly Ser Ala Gly Leu His Arg Arg Arg                         |     |
| 5 10  |     |

## (2) INFORMATION FOR SEQ ID NO: 219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..240
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 99..194  
id N28787  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..95  
id N28787  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 207..280  
id N28787  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 114..208

id AA102327  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 59..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 30..110  
id AA102327  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 31..63
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..33  
id AA102327  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 277..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 250..284  
id AA102327  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..240
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 101..196  
id AA019783  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 209..282  
id AA019783  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 37..97  
id AA019783  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..240
- (C) IDENTIFICATION METHOD: blastn



(D) OTHER INFORMATION: identity 95  
region 115..210  
id AA059290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 41..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 13..111  
id AA059290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 253..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 223..289  
id AA059290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 145..240  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 102..197  
id H86516  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 253..326  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 210..283  
id H86516  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 75..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 34..98  
id H86516  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 171..323  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.6  
seq PALILLFALGSLG/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

```

GGTGCTGTTG CCATCATGGC TGACCCCGAC CCCCGGTACC CTCGCTCCTC GATCGAGGAC 120
GACTTCAACT ATGGCAGCAA GCGTKGGCYT CSGCCACCGT GCACATCCGA ATG GCC 176
                                         Met Ala
                                         -50

TTT CTG AGA AAA GTC TAC AGC ATT CTT TCT CTG CAG GTT CTC TTA ACT 224
Phe Leu Arg Lys Val Tyr Ser Ile Leu Ser Leu Gln Val Leu Leu Thr
          -45                      -40                      -35

ACA GTG ACT TCA ACA GTT TTT TTA TAC TTT GAG TCT GTA CGG ACA TTT 272
Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser Val Arg Thr Phe
          -30                      -25                      -20

GTA CAT GAG AGT CCT GCC TTA ATT TTG CTG TTT GCC CTC GGA TCT CTG 320
Val His Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly Ser Leu
          -15                      -10                      -5

GGT TCG GGG 329
Gly Ser Gly
      1

```

## (2) INFORMATION FOR SEQ ID NO: 220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..180  
id W88492  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 25..111
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq PTLAIALAANAWA/FV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```

ACCATATGGG TGGTGTGGAT CGTC ATG TAT ACT TAC GGC AAC AAG CAG CAC 51
Met Tyr Thr Tyr Gly Asn Lys Gln His
          -25

```

```

AAC AGT CCC ACC TGG GAT GAC CCC ACG CTG GCC ATC GCC CTC GCC GCC      99
Asn Ser Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile Ala Leu Ala Ala
-20                      -15                      -10                      -5

AAT GCC TGG GCC TTC GTC CTC TTC TAC GTC ATC CCC GAG GTC TCC CAG      147
Asn Ala Trp Ala Phe Val Leu Phe Tyr Val Ile Pro Glu Val Ser Gln
                      1                      5                      10

GTG ACC AAG TCC AGC CCA GAG CAA AGC TAC CAG GGG GAC ATG TAC CCC      195
Val Thr Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly Asp Met Tyr Pro
                      15                      20                      25

ACC CGG GAC TTG                                                    207
Thr Arg Asp Leu
30

```

## (2) INFORMATION FOR SEQ ID NO: 221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(136..167)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 239..270  
id H62766  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 70..165
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq WILVLALPLTVWP/WL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

```

ACTTTCAGTT TCCTTCTTCC AGCACGGAGT AACTGCTCT GCCTCCACTT AGATTACTTC      60

AGAAATGAA ATG CAG CAA ATA TTT ATC CAG CAG TGC AGG GAG TTG AAC TTT      111
Met Gln Gln Ile Phe Ile Gln Gln Cys Arg Glu Leu Asn Phe
-30                      -25                      -20

TGG AGT CGG GAA CCT TGG ATT CTT GTT CTG GCT CTG CCA CTT ACT GTG      159
Trp Ser Arg Glu Pro Trp Ile Leu Val Leu Ala Leu Pro Leu Thr Val
-15                      -10                      -5

```

TGG CCT TGG CTC TCC CCG GAG GCT CAG CCC CCT CTG 195  
Trp Pro Trp Leu Ser Pro Glu Ala Gln Pro Pro Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 308..370  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 404..466  
id AA158879  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 110..154  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.5  
seq AVLLALLMAGLAL/OP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

AACTGGCTCC AGGAAACCCG CTGGTGTGA CTGTGGGCAG TCCAGCCTCT CCCCATTTGA 60

GGCCATATAA ANNACCTGAG GCCCTCTCCA CCACAGCCCA CCAGTGACC ATG AAG GCT 118  
Met Lys Ala  
-15

GTG CTG CTT GCC CTG TTG ATG GCA GGC TTG GCC CTG CAG CCA GGC ACT 166  
Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln Pro Gly Thr  
-10 -5 1

GCC CTG CTG TGC TAC TCC TGG ARR GCC CAG GTG RGC AAC GAG GAC TGC 214  
Ala Leu Leu Cys Tyr Ser Trp Xaa Ala Gln Val Xaa Asn Glu Asp Cys  
5 10 15 20

CTG CAG GTG GAG AAC TGC ACC CAG CTG GGG GAG CAG TGC TGG ACC GCG 262  
Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys Trp Thr Ala  
25 30 35

CGC ATC CGC GCA GTT GGC CTC CTG ACC GTC ATC AGC AAA GGC TGC AGC 310  
Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys Gly Cys Ser  
40 45 50

TTG AAC TGC GTG GAT SAC TCA CAG GAC TAC TAC GTG GGC AAG AAG AAC 358  
 Leu Asn Cys Val Asp Xaa Ser Gln Asp Tyr Tyr Val Gly Lys Lys Asn  
           55                                60                                65

ATC ACG TGC TGT GAC 373  
 Ile Thr Cys Cys Asp  
           70

## (2) INFORMATION FOR SEQ ID NO: 223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
                                 region 1..247  
                                 id AA166578  
                                 est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 4..51
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
                                 seq QACLLGLFALILS/GK

## -(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

AGA ATG GGA CTC CAA GCC TGC CTC CTA GGG CTC TTT GCC CTC ATC CTC 48  
 Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu  
           -15                                -10                                -5

TCT GGC AAA TGC AGT TAC AGC CCG GAG CCC GAC CAG CGG AGG ACG CTG 96  
 Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr Leu  
           1                                5                                10                                15

CCC CCA GGC TGG GTG TCC CTG GGC CGT GCG GAC CCT GAG GAA GAG CTG 144  
 Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu Glu Leu  
                                 20                                25                                30

AGT CTC ACC TTT GCC CTG AGA CAG CAG AAT GTG GAA AGA CTC TCG GAG 192  
 Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg Leu Ser Glu  
           35                                40                                45

CTG GTG CAG GCT GTG TCG GAT CCC AGC TCT CCT CAA TAC GGA AAA TAC 240

Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln Tyr Gly Lys Tyr  
50 55 60

CTG ACC CGT  
Leu Thr Arg  
65

249

## (2) INFORMATION FOR SEQ ID NO: 224:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(141..361)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 146..366  
id H19708  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 143..264  
id H20045  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 4..77  
id H20045  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 8..247  
id C15772  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 157..341  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 1..185  
                           id H67240  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 340..382  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 185..227  
                           id H67240  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 172..382  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 1..211  
                           id HUM408E11B  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 2..88  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7  
                           seq LGSGLGLSPGTSS/GR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

|   |     |
|---|-----|
| G ATG AGG CCG GGG CAG GTC TCC CTC CTG GGT CCT GAT GCT GTT TCT GTG | 49  |
| Met Arg Pro Gly Gln Val Ser Leu Leu Gly Pro Asp Ala Val Ser Val   |     |
| -25 -20 -15   |     |
| CTC GGC TCT GGC TTG GGC CTC AGC CCT GGC ACC AGC TCT GGC CGC AAC   | 97  |
| Leu Gly Ser Gly Leu Gly Leu Ser Pro Gly Thr Ser Ser Gly Arg Asn   |     |
| -10 -5 1  |     |
| CCT GAC CCT GGC TCT GGG CCG GGC ACT CTG CCG GRT YCC AGC DTC CAA   | 145 |
| Pro Asp Pro Gly Ser Gly Pro Gly Thr Leu Pro Xaa Xaa Ser Xaa Gln   |     |
| 5 10 15   |     |
| AAC CCC TCC CCG GCT CCA GAT CCA CCC CCA GCC CTA CTC CTG TGG AAT   | 193 |
| Asn Pro Ser Pro Ala Pro Asp Pro Pro Pro Ala Leu Leu Leu Trp Asn   |     |
| 20 25 30 35   |     |
| CTT CTG ACC CAA AGG CTG GGC ACG ACG CTG GTC CCG ACC TTG TGC CCA   | 241 |
| Leu Leu Thr Gln Arg Leu Gly Thr Thr Leu Val Pro Thr Leu Cys Pro   |     |
| 40 45 50  |     |
| GCC CAG ACC TTG ATC CTG TGC CCA GCC CAG ACC CTG ATC CTG TGC CCA   | 289 |
| Ala Gln Thr Leu Ile Leu Cys Pro Ala Gln Thr Leu Ile Leu Cys Pro   |     |
| 55 60 65  |     |
| RCC CTG ATC CCA ACC CTG TGT CCT GCC CTG AMC CCT GTT CTC CCA STC   | 337 |
| Xaa Leu Ile Pro Thr Leu Cys Pro Ala Leu Xaa Pro Val Leu Pro Xaa   |     |

70

75

80

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTG | GCA | CTG | TCA | GCC | CAG | CCC | TCC | CTA | CCG | GCG | AGA | GTC | CAG | AGT | 382 |
| Val | Ala | Leu | Ser | Ala | Gln | Pro | Ser | Leu | Pro | Ala | Arg | Val | Gln | Ser |     |
| 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..139)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 135..272  
id HSB82C022  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 10..108
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8  
seq FTSASLLLLPMSTG/MP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATTATTTAT | ATG | ATT | AAC | CCC | TCA | GTC | CCT | AGC | AAG | TCA | AAT | TCC | CAT | CCG | 51  |     |
| Met       | Ile | Asn | Pro | Ser | Val | Pro | Ser | Lys | Ser | Asn | Ser | His | Pro |     |     |     |
|           |     |     | -30 |     |     |     |     | -25 |     |     |     |     |     | -20 |     |     |
|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| TTT       | TTA | TCT | ACA | GTA | ATG | TTC | ACC | TCT | GCA | TCA | CTG | CTG | CTT | CCC | ATG | 99  |
| Phe       | Leu | Ser | Thr | Val | Met | Phe | Thr | Ser | Ala | Ser | Leu | Leu | Leu | Pro | Met |     |
|           |     |     | -15 |     |     |     |     | -10 |     |     |     |     |     | -5  |     |     |
|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| TCT       | ACA | GGC | ATG | CCA | ACT | CAA | AAC | TGT | TTT | ACC | CCA | AAG |     |     |     | 138 |
| Ser       | Thr | Gly | Met | Pro | Thr | Gln | Asn | Cys | Phe | Thr | Pro | Lys |     |     |     |     |
|           |     |     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE



(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 138..186

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 91  
region 14..62  
id AA111755  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 83..286

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.7  
seq IACLAWWIGGGSG/XN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```

AAAGACTTTG CGAASGCTGC GCTCGCGCCC GGATCCCTCA GCGGCTGCA GGCTTCAGCC      60
TGCGCTGGTT GGTGAAACAG AG ATG TCA GAA AAG GAG AVC AAC TTC CCG CCA      112
               Met Ser Glu Lys Glu Xaa Asn Phe Pro Pro
               -65                               -60

CTG CCC AAG TTC ATC CCT GTG AAG CCC TGC TTC TAC CAG AAC TTC TCC      160
Leu Pro Lys Phe Ile Pro Val Lys Pro Cys Phe Tyr Gln Asn Phe Ser
               -55                               -45

GAC GAG ATC CCA GTG GAG CAC CAG GTC CTG GTG AAG AGG ATC TAC CGG      208
Asp Glu Ile Pro Val Glu His Gln Val Leu Val Lys Arg Ile Tyr Arg
               -40                               -30

CTG TGG ATG TTT TAC TGC GCC ACC CTC GGC GTC AAC CTC ATT GCC TGC      256
Leu Trp Met Phe Tyr Cys Ala Thr Leu Gly Val Asn Leu Ile Ala Cys
               -25                               -15

CTG GCC TGG TGG ATC GGC GGA GGC TCG GGG NNB AAC TTC GGC CTG GCC      304
Leu Ala Trp Trp Ile Gly Gly Gly Ser Gly Xaa Asn Phe Gly Leu Ala
               -10                               -5                               1                               5

TTC GTG TGG CTG CTC CTG TTC ACG CCT TGC GGC TAC GTG TGC TGG TTC      352
Phe Val Trp Leu Leu Leu Phe Thr Pro Cys Gly Tyr Val Cys Trp Phe
               10                               15                               20

CGG CCT GTC TAC AAG GCC TTC CGA GCC GAC AGC TCC TTT AAT TTC ATG      400
Arg Pro Val Tyr Lys Ala Phe Arg Ala Asp Ser Ser Phe Asn Phe Met
               25                               30                               35

GCG CTG
Ala Leu
               40

```

## (2) INFORMATION FOR SEQ ID NO: 227:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(68..131)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 392..455  
id W22335  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 288..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 9..68  
id H70453  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 159..227
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq ILRLYFFFLQLAHS/GY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

```

ACGAAATGGT ATTGACATCT TGGTTGGAAC ACCTGGTCGT ATCAAAGACC ATCTGCAGAG   60
TGGCCGATTG GATCTTTCTA AACTGCGACA TGTTGTGCTT GATGAAGTGG ATCAGATGTT  120
AGATTTAGGT TTCGCTGAAC AAGTTGAAGA TATTATTC ATG AAT CCT ACA AAA CTG   176
                               Met Asn Pro Thr Lys Leu
                               -20
ATT CTG AAG ACA ATC CTC AGA CTT TAC TTT TTT CTG CAA CTT GCC CAC   224
Ile Leu Lys Thr Ile Leu Arg Leu Tyr Phe Phe Leu Gln Leu Ala His
   -15                               -10                               -5
AGT GGG TAT ACA AAG TTG CAA AAA AAA TAC ATG AAA TCC AGA TAT GAA   272
Ser Gly Tyr Thr Lys Leu Gln Lys Lys Tyr Met Lys Ser Arg Tyr Glu
    1               5               10               15
CAG GTT GAC CTT GTT GGR AAA ATG WCT CAA AAG GCT GCA ACT ACT GTG   320

```

Gln Val Asp Leu Val Gly Lys Met Xaa Gln Lys Ala Ala Thr Thr Val  
20 25 30

GRA CAT TTG GCC ATC CAG TGT CAT TGG  
Xaa His Leu Ala Ile Gln Cys His Trp  
35 40

347

## (2) INFORMATION FOR SEQ ID NO: 228:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..70
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..59  
id AA013305  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 197..250
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 189..242  
id AA013305  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 250..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 243..290  
id AA013305  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..199
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 236..299  
id R48472  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 37..101  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 135..199  
 id R48472  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 38..106  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.7  
 seq SXXCFVSVPPASA/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

```

AACCCGGGAC CGAGCTGGGG TCTTGGAGGA AGAGAGG ATG GCG TCG TCG AGC CCT    55
                                     Met Ala Ser Ser Pro
                                     -20

GAC TCC CCA TGT TCC TGS NAC TGC TTT GTC TCC GTG CCC CCG GCC TCA    103
Asp Ser Pro Cys Ser Xaa Xaa Cys Phe Val Ser Val Pro Pro Ala Ser
   -15                               -10                               -5

GCC ATC CCG GST GTG AKC TTK GCC NNH AAC TCG GAC SGA CCC CGG GAC    151
Ala Ile Pro Xaa Val Xaa Xaa Ala Xaa Asn Ser Asp Xaa Pro Arg Asp
   1                               5                               10                               15

GAG GTG CAG GAG GTG GTG TTT GTC CCC GCA GGC ACT CAC ACT CCT GGG    199
Glu Val Gln Glu Val Val Phe Val Pro Ala Gly Thr His Thr Pro Gly
               20                               25                               30

AGC CGG CTC CAG TGC ACC TAC ATT GAA GTG GAA CAG GTG TCG AAG ACG    247
Ser Arg Leu Gln Cys Thr Tyr Ile Glu Val Glu Gln Val Ser Lys Thr
               35                               40                               45

CAC GCT GTG ATT CTG AGC CGT CCT TCT TGG CTA TGG GGG GCT GAG ATG    295
His Ala Val Ile Leu Ser Arg Pro Ser Trp Leu Trp Gly Ala Glu Met
   50                               55                               60

GGC GMV ACG AGC ATG GTG TCT GCA TTG GCA ACG AGG CTG TGT GGA CGA    343
Gly Xaa Thr Ser Met Val Ser Ala Leu Ala Thr Arg Leu Cys Gly Arg
   65                               70                               75

AGG AGC CAG TTG GGG AGG GCN GKN GCC CTS CTG GGC ATG GAC CTA CTC    391
Arg Ser Gln Leu Gly Arg Ala Xaa Ala Leu Leu Gly Met Asp Leu Leu
   80                               85                               90                               95

AGG TGC AGA CCC TGC    406
Arg Cys Arg Pro Cys
               100
  
```

## (2) INFORMATION FOR SEQ ID NO: 229:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 128..197  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 97  
                            region 158..227  
                            id AA249540  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 241..309  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 92  
                            region 267..335  
                            id AA249540  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 164..240  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 97  
                            region 58..134  
                            id N46699  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 128..161  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 100  
                            region 23..56  
                            id N46699  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: complement(224..309)  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 96  
                            region 104..189  
                            id W39777  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 233..309  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 96  
                            region 13..89  
                            id AA036848  
                            est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 233..309  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 13..89  
id AA133513  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 171..287  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq XLIAXLEPPGAMA/VR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

```
CATTATTCCT TTTCCATCGG AAGTGGCGCT CGTGCATTCA ACTTGTTCCC GTCATGGAA    60
CCCCTCTTTA AAAAGACGCA GGGCACCTGT GAGCGCAGGA GCGAGCCTAA GGCCACCCAG   120
CGGCAGCGCC CGTGTCTTGG GCACTCAGCG TGCTGGGCAG AGCAGGTGCG ATG GSC      176
                                     Met Xaa
CCA GTC CTA GCA GCC CTC GCC CAT GTC CTG TGC CCT TAC ATG GCT CCC      224
Pro Val Leu Ala Ala Leu Ala His Val Leu Cys Pro Tyr Met Ala Pro
   -35                      -30                      -25
GGA CTG TGC AGG GAG CCG ATA CGT TTK CTG ATA GCA VTA CTG GAA CCA      272
Gly Leu Cys Arg Glu Pro Ile Arg Xaa Leu Ile Ala Xaa Leu Glu Pro
   -20                      -15                      -10
CCG GGT GCG ATG GCA GTK AGG AGA CTG CCC AGT GCC                        308
Pro Gly Ala Met Ala Val Arg Arg Leu Pro Ser Ala
   -5                      1                      5
```

## (2) INFORMATION FOR SEQ ID NO: 230:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..327  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..309

id C16848  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..104
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 303..332  
id R40385  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 73..207
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq PMLGLAAFRWIWS/RE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```

AAAAGCGGAC CCGCGGACGG TGGCGTTAAG GGAACGCTGA GGTCCCGCGC TCCCCGACCG      60
AGGTATATCT CC ATG AAT AAC CTA AAT GAT CCC CCA AAT TGG AAT ATC CGG      111
           Met Asn Asn Leu Asn Asp Pro Pro Asn Trp Asn Ile Arg
           -45                      -40                      -35

CCT AAT TCC AGG GCG GAT GGT GGT GAT GGA AGC AGG TGG AAT TAT GCC      159
Pro Asn Ser Arg Ala Asp Gly Gly Asp Gly Ser Arg Trp Asn Tyr Ala
           -30                      -25                      -20

CTG TTG GTT CCA ATG CTG GGA TTG GCT GCT TTT CGT TGG ATT TGG TCT      207
Leu Leu Val Pro Met Leu Gly Leu Ala Ala Phe Arg Trp Ile Trp Ser
           -15                      -10                      -5

AGG GAG TCC CAG AAA GAA GTA GAA AAA GAG AGA GAA GCC TAC CGT CGG      255
Arg Glu Ser Gln Lys Glu Val Glu Lys Glu Arg Glu Ala Tyr Arg Arg
           1                      5                      10                      15

AGA ACT GCT GCT TTT CAA CAG GAT CTG GAA GCC AAG TAC CAC GCC ATG      303
Arg Thr Ala Ala Phe Gln Gln Asp Leu Glu Ala Lys Tyr His Ala Met
           20                      25                      30

ATC TCA GAM AAT CGG CGT GCT GTC      327
Ile Ser Xaa Asn Arg Arg Ala Val
           35                      40

```

## (2) INFORMATION FOR SEQ ID NO: 231:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(3..297)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..295  
id W57719  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(37..300)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 10..273  
id H04979  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(7..41)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 270..304  
id H04979  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(37..295)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 7..265  
id H10390  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..41)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 262..301  
id H10390  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(142..295)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..154  
id W42765  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..141)
- (C) IDENTIFICATION METHOD: blastn



(D) OTHER INFORMATION: identity 100  
region 156..295  
id W42765  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(55..238)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 71..254  
id R39116  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(255..297)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 10..52  
id R39116  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 295..351  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.6  
seq AALCSLFFFLSLQ/EI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

```
ACGTTAGGGG GCCAGGGAGA TGTGACTGAG GCTGGCTTTC CACGTGAATG AGACGGGGTC   60
GGTGGAGGGT TTGGTGCTAC AGCCAGTCAG AAGATTGCA AATGCGAACA CATTCTCTGTG  120
TGAGGCACGT TACCCTTTGT CAGTTATTGT GAATATGTGT ATTTTAAGCA ATAAGATTCA  180
GCTGGTCAGA CTTTTCTGGG CAGTCTCAGT GACGCATTTT CTGTGCTGTG ATTGTTCTGA  240
AGACAGAGTG GCTCTAACCA CTGTGAGAAG CCCAAATAAA AATTGATCCC AAAA ATG    297
                                   Met
CTA CTG CTC TTT CTT GCT GCA CTT TGT TCC CTC TTC TTC TTC CTC AGT    345
Leu Leu Leu Phe Leu Ala Ala Leu Cys Ser Leu Phe Phe Phe Leu Ser
      -15                      -10                      -5

CTT CAG GAA ATT GCA CCT CAA GAT CCC AAA CCA GGG                      381
Leu Gln Glu Ile Ala Pro Gln Asp Pro Lys Pro Gly
      1                      5                      10
```

## (2) INFORMATION FOR SEQ ID NO: 232:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..175
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 1..159  
id W51023  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 42..173
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..132  
id T61976  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 2..142
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5  
seq IIVCLFAFLVAHC/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

|   |     |
|---|-----|
| T ATG TTA TTC CTT GGC AAG GTG CTG ATA GTC TGC AGC ACA GGT TTA GCT | 49  |
| Met Leu Phe Leu Gly Lys Val Leu Ile Val Cys Ser Thr Gly Leu Ala   |     |
| -45 -40 -35   |     |
| GGG ATT ATG CTG CTC AAC TAC CAG CAG GAC TAC ACA GTA TGG GTG CTG   | 97  |
| Gly Ile Met Leu Leu Asn Tyr Gln Gln Asp Tyr Thr Val Trp Val Leu   |     |
| -30 -25 -20   |     |
| CCT CTG ATC ATC GTC TGC CTC TTT GCT TTC CTA GTC GCT CAT TGC TTC   | 145 |
| Pro Leu Ile Ile Val Cys Leu Phe Ala Phe Leu Val Ala His Cys Phe   |     |
| -15 -10 -5 1  |     |
| CTG TCT ATT TAT GAA ATG GTA GTK GAT GCG AGG                       | 178 |
| Leu Ser Ile Tyr Glu Met Val Val Asp Ala Arg                       |     |
| 5 10  |     |

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: complement(2..321)  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 100  
                            region 59..378  
                            id AA045815  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 95..244  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 1..150  
                            id R18658  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 240..321  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 100  
                            region 147..228  
                            id R18658  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 95..321  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 100  
                            region 1..227  
                            id R14615  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: complement(2..200)  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 100  
                            region 3..201  
                            id N95174  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: complement(36..197)  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 98  
                            region 8..169  
                            id N93742  
                            est
- (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..44)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 166..208  
id N93742  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 191..304
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq LLLLVHSFWFTVC/TP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```

AAGACTCATA GAGATTAAAT GATCACTATG GTCCTTCTTC TGTTAAATGG AGCCAAAGAC      60
GCCTATGTTG TTCTGAAGTC TTGTAATGTT TAACTTCTGA GAACTTAGAT TAGTGGTGTG     120
ATGATAGAGT CTGTATAACG CATTGAAAAG GGTATCAGGC TTAGTTATTT ATCCAATAAA     180
TATTTATTGT ATG CAG GGT ATT CCT ATT TTA ACT CCT GTG ACA ACA CAA         229
      Met Gln Gly Ile Pro Ile Leu Thr Pro Val Thr Thr Gln
                -35                                -30

AGC ATA GCG ATT TCC ATA GTT CTA ACT GTT CAG GGT CTG CTC CTC CTG         277
Ser Ile Ala Ile Ser Ile Val Leu Thr Val Gln Gly Leu Leu Leu Leu
-25                -20                                -15                                -10

GTA CAC TCT TTT TGG TTC ACT GTA TGT ACT CCT GTT GTC TTT                 319
Val His Ser Phe Trp Phe Thr Val Cys Thr Pro Val Val Phe
                -5                                1                                5

```

## (2) INFORMATION FOR SEQ ID NO: 234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(131..360)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 45..274  
id M78402  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(57..234)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 10..187  
id H04786  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(7..43)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 201..237  
id H04786  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(57..234)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 10..187  
id H17078  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(7..43)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 201..237  
id H17078  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(57..217)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..161  
id HSC0UC022  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..43)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 175..217  
id HSC0UC022  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 199..279
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq LFCVLLSLRPHTS/GT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```

ACAAGATTTT CCAACCTTGC TGGCTACTTT AGTTTGGGAC CTGTTTTTTT TCTCATTGA      60
TTTTGCTTGT GCAGAAAATA GTTTCAGCA CATGGATTGA TCTGAGAGAG AATGAGGCTC     120
AGTTGTGGAT AGTCTGTTTT CTCTGAGCAT GTTGGCCAAC TAGTATCGTC AAATTATTGA     180
GTGGATCATC TCTTGGAATG CAG AAC TTC TGC CAC CAC TTG GCT ATT TGC         231
              Met Gln Asn Phe Cys His His Leu Ala Ile Cys
              -25                               -20

ACA GTC ATC TTG TTC TGT GTC CTT TTA TCT CTC AGA CCA CAC ACA TCT       279
Thr Val Ile Leu Phe Cys Val Leu Leu Ser Leu Arg Pro His Thr Ser
-15                               -10                               -5

GGA ACG CTG TGG GCA TCT TCT GCC CAT GGG CTC CAT TTG GCA CCT GCT       327
Gly Thr Leu Trp Ala Ser Ser Ala His Gly Leu His Leu Ala Pro Ala
  1                               5                               10                               15

GAG CCA CAG TTG TCC TGC TGG ATG TGC TGT GCA                           360
Glu Pro Gln Leu Ser Cys Trp Met Cys Cys Ala
      20                               25

```

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

-(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 35..326  
id H97426  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 92..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 14..238  
id W44834  
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 127..177  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 4..54  
 id R57989  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 182..211  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 62..91  
 id R57989  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(287..316)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 385..414  
 id N93806  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 34..225  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.3  
 seq VLMRLVASAYSIA/QK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

|  |     |
|--|-----|
| AAGTTTCCCG CATGCTCAGT AGCTGAGGTA GGG ATG CCA TCC TTC TCA AAA GAC | 54  |
| Met Pro Ser Phe Ser Lys Asp                                      |     |
| -60  |     |
| TTA TTG ACA GTG CCA AAG CTC GGT ACT GGA CAC VMC GRR GGR MCT GGG  | 102 |
| Leu Leu Thr Val Pro Lys Leu Gly Thr Gly His Xaa Xaa Gly Xaa Gly  |     |
| -55 -50 -45  |     |
| TCC TAC GAT RAC GCG CTT KTG CTC CTC CTG AAG TGT CTT TGG TCC AAC  | 150 |
| Ser Tyr Asp Xaa Ala Leu Xaa Leu Leu Leu Lys Cys Leu Trp Ser Asn  |     |
| -40 -35 -30  |     |
| GTT GTT CCA GAG TGT ACC ATG GCT TCC AGT AAC ACT GTG TTG ATG CGG  | 198 |
| Val Val Pro Glu Cys Thr Met Ala Ser Ser Asn Thr Val Leu Met Arg  |     |
| -25 -20 -15 -10  |     |
| TTG GTA GCC TCC GCA TAT TCT ATT GCT CAA AAG GCA GGA ATG ATA GTC  | 246 |
| Leu Val Ala Ser Ala Tyr Ser Ile Ala Gln Lys Ala Gly Met Ile Val  |     |
| -5 1 5   |     |
| AGA CGT GTT ATT GCT GAA GGA GAC CTG GGT ATT GTG GAG AAG ACC TGT  | 294 |
| Arg Arg Val Ile Ala Glu Gly Asp Leu Gly Ile Val Glu Lys Thr Cys  |     |
| 10 15 20   |     |
| GCA ACA GAC CTG CAG ACC AAA GCT GAC CGA TTG GCA CAG ATG AGC ATA  | 342 |
| Ala Thr Asp Leu Gln Thr Lys Ala Asp Arg Leu Ala Gln Met Ser Ile  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 25  |     |     |     | 30  |     |     |     | 35  |     |     |     |     |     |     |     |     |
| TGT | TCT | TCA | TTG | GYM | BGG | AAA | TTC | CCC | AAA | CTC | RNR | ATT | ATA | GGG | GAA | 390 |
| Cys | Ser | Ser | Leu | Xaa | Xaa | Lys | Phe | Pro | Lys | Leu | Xaa | Ile | Ile | Gly | Glu |     |
| 40  |     |     |     |     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GAG | GAT | CTG | CCT | TCT | GAG | GAA | GTG | GAT | CAA | GAG | CTG | ATT | GAA | GAC | AGK | 438 |
| Glu | Asp | Leu | Pro | Ser | Glu | Glu | Val | Asp | Gln | Glu | Leu | Ile | Glu | Asp | Xaa |     |
|     |     |     |     | 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |     |

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 7..113  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 15..121  
id W04921  
est

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- [illegible]



## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(32..113)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 359..440  
id N70602  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(261..311)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 164..214  
id N70602  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(213..259)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 215..261  
id N70602  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 114..194
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 59..139  
id W70167  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 238..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 183..256  
id W70167  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..59  
id W70167  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..236
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 139..182

id W70167  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 221..311  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 165..255  
id W37690  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 114..187  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 58..131  
id W37690  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 56..113  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..58  
id W37690  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 185..220  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 130..165  
id W37690  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 227..289  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.2  
seq LEMLXAFASHIXA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

```
ATGGCAGCTT CCTTGGCTCG GCTTGGTCTG CGGCCTGTCA AACAGGTTTC GGTTCAGTTC    60
TGTCCTTCG AGAAAAACGT GGAATCGACG AGGACCTTCV TSCAGACGGT GAGGCMGTGA    120
GAAGGTCCGC TCCACTAATC TCAACTGCTC AGTGATTGCG GACGTGASGC ATGACGGCTC    180
CGAGCCCTGC GTGGACGTGC TGTTCCGAGA CGGGCATCGC CTGATT ATG CGC GGC        235
                                   Met Arg Gly
                                   -20
GCT CAT CTC ACC GCT CTG GAA ATG CTC ANM GCC TTC GCC TCC CAC ATM        283
Ala His Leu Thr Ala Leu Glu Met Leu Xaa Ala Phe Ala Ser His Ile
```

-15

-10

-5

HGG GCC AGG GAC GCG GCG GGC AGC GGG  
Xaa Ala Arg Asp Ala Ala Gly Ser Gly  
1 5

310

## (2) INFORMATION FOR SEQ ID NO: 237:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 321..431
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 186..296  
id AA043558  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 218..299
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 83..164  
id AA043558  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 39..96  
id AA043558  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..299
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 57..225  
id N50523  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 321..431

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 247..357  
id N50523  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(45..115)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..71  
id N50523  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(321..431)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 289..399  
id AA115605  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(217..318)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 403..504  
id AA115605  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(166..231)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 491..556  
id AA115605  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 172..318  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 36..182  
id AA115129  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 321..431  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 186..296  
id AA115129  
est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 174..318  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
 region 41..185  
 id AA035548  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 325..431  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
 region 194..300  
 id AA035548  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 7..423  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.2  
 seq FGLLHQLSQCVTS/LE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

|   |     |
|---|-----|
| ACAAGG ATG GAA GTG GGC TTA CCG GCC ATT ACC CTC TTT CTC ACC AGC  | 48  |
| Met Glu Val Gly Leu Pro Ala Ile Thr Leu Phe Leu Thr Ser         |     |
| -135 -130   |     |
| GCC AGC AGC CCT GTG GTG GCG ACG ACG ATG GAC CAG GAG CCA GTG GGC | 96  |
| Ala Ser Ser Pro Val Val Ala Thr Thr Met Asp Gln Glu Pro Val Gly |     |
| -125 -120 -115 -110   |     |
| GGT GTG GAA CGA GGA GAA GCC GTC GCA GCC TCG GGA RCT GCG GCC GCC | 144 |
| Gly Val Glu Arg Gly Glu Ala Val Ala Ala Ser Gly Xaa Ala Ala Ala |     |
| -105 -100 -95   |     |
| GCG GCA TTC GGG GAA TCT GCA GGG CAG ATG AGT AAC GAA AGA GGC TTT | 192 |
| Ala Ala Phe Gly Glu Ser Ala Gly Gln Met Ser Asn Glu Arg Gly Phe |     |
| -90 -85 -80   |     |
| GAA AAT GTA GAA CTG GGA GTC ATA GGA AAA AAG AAG AAA GTC CCA AGG | 240 |
| Glu Asn Val Glu Leu Gly Val Ile Gly Lys Lys Lys Lys Val Pro Arg |     |
| -75 -70 -65   |     |
| AGA GTC ATC CAC TTT GTT AGT GGT GAA ACA ATG GAA GAA TAT AGC ACA | 288 |
| Arg Val Ile His Phe Val Ser Gly Glu Thr Met Glu Glu Tyr Ser Thr |     |
| -60 -55 -50   |     |
| GAT GAA GAC GAH GTT GAT GGC CTG GAG AAG NNG ATG TTT TGC CTA CTG | 336 |
| Asp Glu Asp Xaa Val Asp Gly Leu Glu Lys Xaa Met Phe Cys Leu Leu |     |
| -45 -40 -35 -30   |     |
| TTG ATC CGR CAA AAC TTA CCT GGG GTC CCT ACT TAT GGT TTT ACA TGC | 384 |
| Leu Ile Arg Gln Asn Leu Pro Gly Val Pro Thr Tyr Gly Phe Thr Cys |     |
| -25 -20 -15   |     |
| TTC GGG CTG CTA CAT CAA CTC TCT CAG TGT GTG ACT TCC TTG GAG     | 429 |
| Phe Gly Leu Leu His Gln Leu Ser Gln Cys Val Thr Ser Leu Glu     |     |

## (2) INFORMATION FOR SEQ ID NO: 238:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 31..251  
id T34679  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 104..250  
id N34677  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..170
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 21..98  
id N34677  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 203..335  
id N32531  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 202..334  
id N36824

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..170
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 28..96  
id N36824  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 175..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 100..237  
id H97539  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 151..279
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1  
seq SAATLASLGGTSS/RR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

```

AACTCTCGTG CCAAGCATGT CTCTCCAAAT GGCTGCTCTC TGGCGTTCCT CACACTCCCC    60
CTGAAGTTCA TCTAAGATCT TCATTCTTCA WAGGCGGAAG CCCGGCTCGC TGCAAAACGG    120
GCGGCCCGCG CGGAGGCTCG CGAGATCCGC ATG AAG GAG CTG GAG CGG CAG CAG    174
                Met Lys Glu Leu Glu Arg Gln Gln
                -40

AAG GAG GTA GAA GAG AGA CCA GAA AAA GAT TTT ACT GAG AAG GGG TCT    222
Lys Glu Val Glu Glu Arg Pro Glu Lys Asp Phe Thr Glu Lys Gly Ser
-35                -30                -25                -20

CGT AAC ATG CCG GGC CTG TCT GCA GCC ACG CTG GCC TCT CTG GGT GGG    270
Arg Asn Met Pro Gly Leu Ser Ala Ala Thr Leu Ala Ser Leu Gly Gly
                -15                -10                -5

ACT TCC TCT CGG AGA GGC AGC GGA GAC ACC TCC ATC TCC ATC GAC CCC    318
Thr Ser Ser Arg Arg Gly Ser Gly Asp Thr Ser Ile Ser Ile Asp Pro
                1                5                10

GAG    321
Glu

```

## (2) INFORMATION FOR SEQ ID NO: 239:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 270..403

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92  
region 199..332  
id AA125491  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 70..135

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 1..66  
id AA125491  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement (27..135)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 89..197  
id HSB72F052  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(135..223)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 2..90  
id HSB72F052  
est

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: 126..188

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.1  
seq VLVILCIVTVCVT/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

ACCGGAGAAA AAATGGTTCA TGGAGCCTGC GGTTATTGTT TGCCTGGGTG GAATTTTACC 60

TTTTGGTTCA ATCTTTATTG AAATGTATTT CATCTTCACG TCTTTCTGGG CATATAAGAT 120

CTATT ATG TCT ATG GGC TTC ATG ATG CTG GTG CTG GTT ATC CTG TGC ATT 170

Met Ser Met Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile

-20

-15

-10



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTG | ACT | GTC | TGT | GTG | ACT | ATT | GTG | TGC | ACA | TAT | TTT | CTA | CTA | AAT | GCA | 218 |
| Val | Thr | Val | Cys | Val | Thr | Ile | Val | Cys | Thr | Tyr | Phe | Leu | Leu | Asn | Ala |     |
| -5  |     |     |     |     |     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GAA | GAT | TAC | AGG | TGG | CAA | TGG | ACA | AGT | TTT | CTC | TCT | GCT | GCA | TCA | ACT | 266 |
| Glu | Asp | Tyr | Arg | Trp | Gln | Trp | Thr | Ser | Phe | Leu | Ser | Ala | Ala | Ser | Thr |     |
|     |     |     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GCA | ATC | TAT | GTT | TAC | ATG | TAT | TCC | TTT | TAC | TAC | TAT | TTT | TTC | AAA | ACA | 314 |
| Ala | Ile | Tyr | Val | Tyr | Met | Tyr | Ser | Phe | Tyr | Tyr | Tyr | Phe | Phe | Lys | Thr |     |
|     |     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| AAG | ATG | TAT | GGC | TTA | TTT | CAA | ACA | TCA | TTT | TAC | TTT | GGA | TAT | ATG | GCG | 362 |
| Lys | Met | Tyr | Gly | Leu | Phe | Gln | Thr | Ser | Phe | Tyr | Phe | Gly | Tyr | Met | Ala |     |
|     |     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GTA | TTT | AGC | ACA | GCC | TTG | GGG | ATA | ATG | TGT | GGA | GCG | ATT |     |     |     | 401 |
| Val | Phe | Ser | Thr | Ala | Leu | Gly | Ile | Met | Cys | Gly | Ala | Ile |     |     |     |     |
|     | 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 240:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..397
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 131..375  
id W56159  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..121  
id W56159  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..467
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 303..617

id HSZ78368  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 214..293  
id HSZ78368  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..374
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 80..301  
id AA026570  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..70  
id AA026570  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 372..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 300..333  
id AA026570  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 155..467
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 83..395  
id AA109961  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 20..71  
id AA109961  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..363
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96  
region 274..484  
id AA046907  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 60..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 185..264  
id AA046907  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 128..337  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6  
seq LLFPLTLVRSFWS/DM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```

AACGCTTGCG ATGGTTGAAT TCCCCTCCTC ACGCCAGCCT AGGAGAAGAA GTTCGTAGTC      60
CCAGAGGAAG AGGAGTTGTA CGCATGTCAG AGAGGTTGCA GGCTGTTTTC AATTTGTCAG    120
TTTGTGG ATG ATG GAA TTG GRM CTW AAA AKC GRA ACT AAA KKG GAA TGK      169
    Met Met Glu Leu Xaa Leu Lys Xaa Xaa Thr Lys Xaa Glu Xaa
    -70                      -65                      -60
GAA TCT GCA TGT ACA GAA GCA TAT TCC CAA TCT GAT GAG CAA TAT GCT      217
Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala
    -55                      -50                      -45
TGC CAT CTT GGT TGC CAG AAT CAG CTG CCA TTC GCT GAA CTG AGA CAA      265
Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln
    -40                      -35                      -30                      -25
GAA CAA CTT ATG TCC CTG ATG CCA AAA ATG CAC CTA CTC TTT CCT CTA      313
Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu
    -20                      -15                      -10
ACT CTG GTG AGG TCA TTC TGG AGT GAC ATG ATG GAC TCC GCA CAG AGC      361
Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser
    -5                      1                      5
TTC AKA ACC TCT TCA TGG ACT TTT TAT CTT CAA GCC GAT GMC GGM MAA      409
Phe Xaa Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Xaa Gly Xaa
    10                      15                      20
ATA GTT ATA TKC CAG TCT AAG CCA GAA ATC CAG TAC GCA CCA CAT TTG      457
Ile Val Ile Xaa Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu
    25                      30                      35                      40
GAG CAG GAG
Glu Gln Glu
466

```

## (2) INFORMATION FOR SEQ ID NO: 241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..81
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 62..125  
id AA092155  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 68..131  
id AA128307  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 68..131  
id N99068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 68..131  
id AA039944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 68..131  
id AA128099  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

- (B) LOCATION: 1..72
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq GLILLFASHLINQ/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

|   |    |
|---|----|
| ATG GTT TCC AAT GCT TCR GAG ACT TCC TGC CTA GGC CTC ATC CTC CTC | 48 |
| Met Val Ser Asn Ala Ser Glu Thr Ser Cys Leu Gly Leu Ile Leu Leu |    |
| -20 -15 -10   |    |

|   |    |
|---|----|
| TTT GCC AGT CAC CTG ATT AAC CAA TTC TCC AGC | 81 |
| Phe Ala Ser His Leu Ile Asn Gln Phe Ser Ser |    |
| -5 1  |    |

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..302
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..274  
id H18735  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..302
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 116..275  
id T80360  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 51..115  
id T80360  
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 29..69  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..41  
id T80360  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 66..302  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..237  
id AA137006  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 301..336  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 412..447  
id AA137006  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 65..302  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 2..239  
id HSC2CA081  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 64..224  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..161  
id T36290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 223..302  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 161..240  
id T36290  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 2..220  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6  
seq LIVFISVCTALLA/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

```

A ATG CCC CGG AAG CGG AAG TGC GAT CTT CGG GCT GTC AGA GTT GGT CTG   49
  Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu
    -70                      -65                      -60

TTA CTC GGT GGT GGC GGA GTC TAC GGA AGC CGT TTT CGC TTC ACT TTT   97
Leu Leu Gly Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
   -55                      -50                      -45

CCT GGC TGT AGA GCG CTT TCC CCC TGG CGG GTG AGA VTG CAG AGA CGA   145
Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg
   -40                      -35                      -30

AGG TGC GAG ATG AGC ACT ATG TTC GCG GAC ACT CTC CTC ATC GTT TTT   193
Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
  -25                      -20                      -15                      -10

ATC TCT GTG TGC ACG GCT CTG CTC GCA GAG GGC ATA ACC TGG GTC CTG   241
Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu
    -5                      1                      5

GTT TAC AGG ACA GAC AAG TAC AAG AGA CTG AAG GCA GAA GTG GAA AAA   289
Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys
    10                      15                      20

CAG AGT AAA AAA TAT TTG ATG GTA GAG TGG TGG CAA ASC TTC CTT TTT   337
Gln Ser Lys Lys Tyr Leu Met Val Glu Trp Trp Gln Xaa Phe Leu Phe
    25                      30                      35

TAC CCC TCT TTC TTA SAT CCA AAG RCT GTC TCA TCG   373
Tyr Pro Ser Phe Leu Xaa Pro Lys Xaa Val Ser Ser
    40                      45                      50

```

## (2) INFORMATION FOR SEQ ID NO: 243:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 159..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 121..269  
id W31320  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..121

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..85  
id W31320  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 320..380  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 282..342  
id W31320  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 114..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 77..128  
id W31320  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 400..443  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 364..407  
id W31320  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 154..307  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 2..155  
id T27259  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 320..443  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 168..291  
id T27259  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 192..307  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 108..223  
id AA157646  
est

(ix) FEATURE:



- (A) NAME/KEY: other
- (B) LOCATION: 64..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..32  
id AA157646  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 320..443
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 123..246  
id AA182962  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..110  
id AA182962  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 243..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 189..253  
id T71690  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 181..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 125..179  
id T71690  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 114..164
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 58..108  
id T71690  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 130..198
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq LGAAALALLLANT/DV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

```

CCCCGCCCCCT GGGACCCTCC GGGCCGGGCG GTTTGGCCCC TTAGCGCCCC GCGTCGGGG      60
CGGTAAAAGG CCGGCAGAAG GGAGGCACTT GAGAAATGTC TTTCTCCAG GACCCAAGTT    120
TTCTTCACC ATG GGG ATG TGG TCC ATT GGT GCA GGA GCC CTG GGG GCT GCT    171
      Met Gly Met Trp Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala
                -20                      -15                      -10

GCC TTG GCA TTG CTG CTT GCC AAC ACA GAC GTG TTT CTG TCC AAG CCC      219
Ala Leu Ala Leu Leu Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro
                -5                      1                      5

CAG AAA GCG GCC CTG GAG TAC CTG GAG GAT ATA GAC CTG AAA ACA CTG      267
Gln Lys Ala Ala Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu
                10                      15                      20

GAG AAG GAA CCA AGG ACT TTC AAA GCA AAG GAG CTA TGG GAA AAA AAT      315
Glu Lys Glu Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn
                25                      30                      35

GGA GCT GTG ATT ATG GCC GTG CGG AGG CCA GGC TGT TTC CTC TGT CGA      363
Gly Ala Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg
                40                      45                      50                      55

GAG GAA GCT GCG GAT CTG TCC TCC CTG AAA AGC ATG TTG GAC CAG CTG      411
Glu Glu Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu
                60                      65                      70

GGC GTC CCC CTC TAT GCA GTG GTA AAG GAG CAA CGG                        447
Gly Val Pro Leu Tyr Ala Val Val Lys Glu Gln Arg
                75                      80

```

## (2) INFORMATION FOR SEQ ID NO: 244:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 13..394  
id C17481  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 379..424  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 390..435  
id C17481  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 68..258  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 72..262  
id T46941  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 1..67  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 6..72  
id T46941  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(149..271)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 1..123  
id R75331  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 257..430  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 42..215  
id W95977  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 278..430  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 5..157  
id R57521  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 255..347  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.9  
seq LPLLLVANAGTAA/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

```

ATGAAAATGG GTGTGCTTAT TTCCACGAAG AGGAAAGAGA AGGACTTGCA AAGATATGTA    60
GGCTTGCCAT TCATTCTCGA TATGAAGACT TCGTAGTGGA TGGCTTCAAT GTGTTATATA    120
ACAAGAAGCC TGTCATATAT CTTAGTGCTG CTGCTAGACC TGGCCTGGGC CAATACCTTT    180
GTAATCAGCT CGGCTTGCCC TTCCCCTGCT TGTGCCGTGT ACCCTGTAAC ACTGTGTTTG    240
GATCCCAGCA TCAG  ATG  GAT  GTT  GCC  TTC  CTG  GAG  ADA  CTG  ATT  AAA  GAT    290
                Met Asp Val Ala Phe Leu Glu Xaa Leu Ile Lys Asp
                -30                      -25                      -20

GAT ATA GAG CGA GGA AGA CTG CCC CTG TTG CTT GTC GCA AAT GCA GGA    338
Asp Ile Glu Arg Gly Arg Leu Pro Leu Leu Leu Val Ala Asn Ala Gly
                -15                      -10                      -5

ACG GCA GCA GTA GGA CAC ACA GAC AAG ATT GGG AGA TTG AAA GAA CTC    386
Thr Ala Ala Val Gly His Thr Asp Lys Ile Gly Arg Leu Lys Glu Leu
                1                      5                      10

TGT GAG CAG TAT GGC ATA TGG CTT CAT GTG GAG GGT GTG AAT    428
Cys Glu Gln Tyr Gly Ile Trp Leu His Val Glu Gly Val Asn
    15                      20                      25

```

## (2) INFORMATION FOR SEQ ID NO: 245:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 3..232  
id HSC1WH101  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 41..169  
id R12437  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 63..104  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..42  
id R12437  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 63..230  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..168  
id R13448  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 165..212  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 36..83  
id T69236  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 180..227  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.8  
seq LFNLLWLALACSP/VW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

```
GTTTGTGGCC GTCCGGCCTC CCTGACATGC AGATTTCAC CCAGAAGACA GAGAAGGAGC   60
CAGTGGTCAT GGAATGGGCT GGGGTCAAAG ACTGGGTGCC TGGGAGCTGA GGCAGCCACC  120
GTTTCAGCCT GGCCAGCCCT CTGGACCCCG AGGTTGGACC CTACTGTGAC ACACCTACC   179
ATG CGG ACA CTC TTC AAC CTC CTC TGG CTT GCC CTG GCC TGC AGC CCT   227
Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
   -15                -10                -5

GTT TGG                               233
Val Trp
  1
```

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 178..331  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 118..271  
id R60406  
est

## (ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 178..316  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 57..195  
id N78477  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 214..312  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.8  
seq FICLQWALPHSEA/GD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```

AAAGGCAGGA CTGACGCAGA ATGACAACGG CAACACGACA AGAAGTCCTT GGCCTCTACC   60
GCAGCATTTT CAGGCTTGCG AGGAAATGGC AGGCGACATC AGGGCAGATG GAAGACACCA   120
TCAAAGAAAA ACAGTACATA CTAAATGAAG CCAGAACGCT GTTCCGGAAA AACAAAAATC   180
TCACGGACAC AGACCTAATT AAACAGTGTA TAG ATG AAT GCA CAG CCA GGA TTG   234
                Met Asn Ala Gln Pro Gly Leu
                -30
AWA TTG GAC TGC ATT ACA AGA TTC CTT ACC CAN GGC CAA TTC ATC TGC   282
Xaa Leu Asp Cys Ile Thr Arg Phe Leu Thr Xaa Gly Gln Phe Ile Cys
-25                -20                -15
CTC CAA TGG GCC TTA CCC CAC TCC GAG GCC GGG GAC TTC GAA GCC AAG   330
Leu Gln Trp Ala Leu Pro His Ser Glu Ala Gly Asp Phe Glu Ala Lys
-10                -5                1                5

```

## (2) INFORMATION FOR SEQ ID NO: 247:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(230..352)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 32..154  
id W60134  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(78..189)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 195..306  
id W60134  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(9..87)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 298..376  
id W60134  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(176..352)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 57..233  
id H64097  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(57..189)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 219..351  
id H64097  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(84..352)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 57..325  
id W00624  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(1..70)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 337..406  
id W00624  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(1..168)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 156..323  
id W67127  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(167..323)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 2..158  
id W67127  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(64..352)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 58..346  
id H10776  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(23..64)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 347..388  
id H10776  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 120..326  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.7  
seq LCRLCLVRLFCC/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

```
ATTTGGGGAG GGGCACTGTC TCTTTTTTCT CTCATTTTTA AAATGAAGTG TTGTTGCCTT   60
TGTATGTGGT TCAACCATCC AGCTCCCAGC TGGCTAAACT TTGCCTCCAG TGGTCAAAG   119
ATG GGA AAA GAG TGG GGT TGG CAG GAG ATG GAA AAC GGA GGT GCC GCC   167
Met Gly Lys Glu Trp Gly Trp Gln Glu Met Glu Asn Gly Gly Ala Ala
      -65                      -55
```



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CCA | GCA | TGG | GGG | GCA | GGT | CCC | CCA | GTC | CAC | CCT | GCC | CCT | CCC | CCT | GTG | 215 |
| Pro | Ala | Trp | Gly | Ala | Gly | Pro | Pro | Val | His | Pro | Ala | Pro | Pro | Pro | Val |     |
|     |     |     | -50 |     |     |     |     | -45 |     |     |     |     | -40 |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GAG | AAG | ACG | CTT | AGT | TGG | GGG | TGT | GGG | TTT | GGG | CTC | CAT | TCT | GGA | TTC | 263 |
| Glu | Lys | Thr | Leu | Ser | Trp | Gly | Cys | Gly | Phe | Gly | Leu | His | Ser | Gly | Phe |     |
|     |     | -35 |     |     |     | -30 |     |     |     |     | -25 |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GGC | GGT | TCC | GGG | GGA | GGG | GTG | GGT | CTG | TGC | CGA | TTA | CTC | TGT | CTT | GTA | 311 |
| Gly | Gly | Ser | Gly | Gly | Gly | Val | Gly | Leu | Cys | Arg | Leu | Leu | Cys | Leu | Val |     |
|     |     | -20 |     |     |     | -15 |     |     |     |     | -10 |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| CGT | TTG | TTC | TGC | TGC | TCT | TCA | ATA | TTG | TAT | CAA | CGC | CAG | AAG |     |     | 353 |
| Arg | Leu | Phe | Cys | Cys | Ser | Ser | Ile | Leu | Tyr | Gln | Arg | Gln | Lys |     |     |     |
|     |     | -5  |     |     | 1   |     |     |     | 5   |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..71
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..50  
id R82719  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..62
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 1..44  
id AA069083  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..52
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 2..34  
id R29193  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 23..52  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 10..39  
id AA158081  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 10..96  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.7  
seq AALLLTATVRLSA/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

AAGTCCAAC ATG GCG GCG CCC AGC GGA GGG TGG AAC GGC GTC GGC GCG AGC 51  
Met Ala Ala Pro Ser Gly Gly Trp Asn Gly Val Gly Ala Ser  
-25 -20

TTG TGG GCC GCG CTG CTC CTC ACT GCC ACA GTC AGA CTT TCA GCT TCT 99  
Leu Trp Ala Ala Leu Leu Leu Thr Ala Thr Val Arg Leu Ser Ala Ser  
-15 -10 -5 1

CCC GGC CCA 108  
Pro Gly Pro

## (2) INFORMATION FOR SEQ ID NO: 249:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 7..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..159  
id R24141  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 178..264  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 173..259  
id R24141  
est

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 258..299  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 254..295  
id R24141  
est

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 4..147  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.7  
seq LLLFFGKLLVVG/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATC | ATG | ATC | GCC | ATC | TAC | GGG | AAG | AAT | TTC | TGT | GTC | TCA | GCC | AAA | AAT | 48  |
| Met | Ile | Ala | Ile | Tyr | Gly | Lys | Asn | Phe | Cys | Val | Ser | Ala | Lys | Asn |     |     |
|     |     |     | -45 |     |     |     |     | -40 |     |     |     |     |     | -35 |     |     |
| GCG | TTC | ATG | CTA | CTC | ATG | CGA | AAC | ATT | GTC | AGG | GTG | GTC | GTC | CTG | GAC | 96  |
| Ala | Phe | Met | Leu | Leu | Met | Arg | Asn | Ile | Val | Arg | Val | Val | Val | Leu | Asp |     |
|     |     |     | -30 |     |     |     |     | -25 |     |     |     |     | -20 |     |     |     |
| AAA | GTC | ACA | GAC | CTG | CTG | CTG | TTC | TTT | GGG | AAG | CTG | CTG | GTG | GTC | GGA | 144 |
| Lys | Val | Thr | Asp | Leu | Leu | Leu | Phe | Phe | Gly | Lys | Leu | Leu | Val | Val | Gly |     |
|     |     | -15 |     |     |     |     | -10 |     |     |     |     | -5  |     |     |     |     |
| GGC | GTG | GGG | GTC | CTG | TCC | TTC | TTT | TTT | TTC | TCC | GGT | CGC | ATC | CCG | GGG | 192 |
| Gly | Val | Gly | Val | Leu | Ser | Phe | Phe | Phe | Phe | Ser | Gly | Arg | Ile | Pro | Gly |     |
|     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| CTG | GGT | AAA | GAC | TTT | AAG | AGC | CCC | CAC | CTC | AAC | TAT | TAC | TGG | CTG | CCC | 240 |
| Leu | Gly | Lys | Asp | Phe | Lys | Ser | Pro | His | Leu | Asn | Tyr | Tyr | Trp | Leu | Pro |     |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| AYC | ATG | ACC | TCC | ATC | CTG | GGG | GCC | TAT | GTC | ATC | GCC | AGY | GGC | TTC | TTC | 288 |
| Xaa | Met | Thr | Ser | Ile | Leu | Gly | Ala | Tyr | Val | Ile | Ala | Ser | Gly | Phe | Phe |     |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| AGC | GTT | TTC | GGC | ATG | TGT | GTG | GAC | ACG | CTC | TTC | CTC | TGC | TTC | CTG | GAA | 336 |
| Ser | Val | Phe | Gly | Met | Cys | Val | Asp | Thr | Leu | Phe | Leu | Cys | Phe | Leu | Glu |     |
|     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| GAC | CTG | GAG | CGG | ACA | ACG | GCT | CCC | TGG | ACG | GCC | CTA | CTA | CAT | GTC | CAA | 384 |
| Asp | Leu | Glu | Arg | Thr | Thr | Ala | Pro | Trp | Thr | Ala | Leu | Leu | His | Val | Gln |     |
|     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

GAG CTT CTA  
Glu Leu Leu  
80

393

## (2) INFORMATION FOR SEQ ID NO: 250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 222..265
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 220..263  
id N89186  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 76..348
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq SVLELIVASVCQS/HI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

```

GCTACTTTCT TTTTCAGTCT TTCGGTGC GG AGAAGGGGAG GAGGCGGGCA GAGGTCTGAA 60
AAAATCGAAT GCCTT ATG GAA AGG AAC TGC AAG GGT TCC TTT GGG GTG ATC 111
      Met Glu Arg Asn Cys Lys Gly Ser Phe Gly Val Ile
      -90                      -85                      -80
AAA GAG GGA GAC ACA GAC ACA GRR GAG ACA AAG GCA AGG AGG ACT GTC 159
Lys Glu Gly Asp Thr Asp Thr Xaa Glu Thr Lys Ala Arg Arg Thr Val
      -75                      -70                      -65
TGG GAG CCA CGC GGG CGA TAC AGT TTC CGA GRM ACG CCG CGT CCC GCC 207
Trp Glu Pro Arg Gly Arg Tyr Ser Phe Arg Xaa Thr Pro Arg Pro Ala
      -60                      -55                      -50
TAT CCT GTT GAA CAG TGC GGA TTT GCG AGG CGC GCC CTG GAG CTG CTA 255
Tyr Pro Val Glu Gln Cys Gly Phe Ala Arg Arg Ala Leu Glu Leu Leu
      -45                      -40                      -35
GAG ATC CGG AAG CAC AGC CCC GAG GTG TGC GAA CCA CCA AAC ATC CCA 303
Glu Ile Arg Lys His Ser Pro Glu Val Cys Glu Pro Pro Asn Ile Pro
      -30                      -25                      -20

```

GTT ACC AGT GTC CTT GAA TTG ATA GTG GCT TCT GTT TGT CAG TCT CAT 351  
 Val Thr Ser Val Leu Glu Leu Ile Val Ala Ser Val Cys Gln Ser His  
 -15 -10 -5 1

ATA AGA ACT ACT 363  
 Ile Arg Thr Thr  
 5

## (2) INFORMATION FOR SEQ ID NO: 251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..243  
id AA211459  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 15..212
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq LYMLAEALPVSHG/AH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

GTGAAGATGA AGCC ATG TTT GTA GAA TAT AGA AAA CAA CTG AAG TTA CTG 50  
 Met Phe Val Glu Tyr Arg Lys Gln Leu Lys Leu Leu  
 -65 -60 -55

TTG GAC AGG CTT GCT CAA GTT TCA CCA GAG TTA CTA CTG GCC TCT GTT 98  
 Leu Asp Arg Leu Ala Gln Val Ser Pro Glu Leu Leu Leu Ala Ser Val  
 -50 -45 -40

CGC AGA GTT TTT AGT TCT ACA CTG CAG AAT TGG CAG ACT ACA CGG TTT 146  
 Arg Arg Val Phe Ser Ser Thr Leu Gln Asn Trp Gln Thr Arg Phe  
 -35 -30 -25

ATG GAA GTT GAA GTA GCA ATA AGA TTG CTG TAT ATG TTG GCA GAA GCT 194  
 Met Glu Val Glu Val Ala Ile Arg Leu Leu Tyr Met Leu Ala Glu Ala  
 -20 -15 -10

CTT CCA GTA TCT CAT GGT GCT CAC TTC TCA GGT GAT GTT TCA AAA GCT 242  
 Leu Pro Val Ser His Gly Ala His Phe Ser Gly Asp Val Ser Lys Ala

|   |    |    |    |     |
|---|----|----|----|-----|
| -5  | 1  | 5  | 10 |     |
| AGT GCT TTG CAG GAT ATG ATG CGA ACT CTG GTA ACA TCA GGA GTC AGC |    |    |    | 290 |
| Ser Ala Leu Gln Asp Met Met Arg Thr Leu Val Thr Ser Gly Val Ser |    |    |    |     |
|   | 15 | 20 | 25 |     |
| GGG   |    |    |    |     |
| Gly   |    |    |    | 293 |

## (2) INFORMATION FOR SEQ ID NO: 252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 155..187
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 95..127  
id H83489  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 326..388
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq IIFLIQWHGVSFQ/EF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

|   |     |
|---|-----|
| AAGTCCCTGT ACAGGGTTTC TGACCTGTGG TAAAAACAGA ATGTCACTTT CTGACAGGCA | 60  |
| CAGTACCCCC AGGATAAACT TGGAACCTCG AGAGGAAATT CACGAAACTC GTGGGGGCAG | 120 |
| GGGTCACAAG GTGCTTGGTG GGGGARAASC TGGAAGACAT ATTGTCCAGG AGAAGGAATG | 180 |
| TCACAAGGAA CTGACAAAAT CAAGTCACGG CGCCTACAAA GATGAGGGGC AGATTCTGGC | 240 |
| TGCCTTTTAA TTTCGTCCTT CACCTGATAT CTGTGCCAGA GAATGATAAA AATCATAATA | 300 |
| AAGGRAATAG YGGAAGAGGA GACTT ATG TTA CTG GGG ACA TCT AAC ATA ATT   | 352 |
| Met Leu Leu Gly Thr Ser Asn Ile Ile                               |     |
| -20 -15   |     |
| ATT TTC CTG ATT CAG TGG CAT GGT TCA GTC TTC CAG GAG TTC           | 394 |
| Ile Phe Leu Ile Gln Trp His Gly Ser Val Phe Gln Glu Phe           |     |
| -10 -5 1  |     |

## (2) INFORMATION FOR SEQ ID NO: 253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 48..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 35..225  
id HSC0CC021  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..49
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..35  
id HSC0CC021  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..212  
id T32119  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 36..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..203  
id T35494  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 13..202  
id HUMHG5097  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 51..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..188  
id AA027882  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 78..137
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq AFVXACVLSLIST/IY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

```
AAGAGTAGGG TGCTGTGGTC TGAGCTAGAG GGTGAAGCTG GCGGASAGGA GGATGGGCGA    60
GCAGTCTGAA TGCCAGA ATG GRT AAC CGT TTT GCT ACA GCA TTT GTA ATD      110
      Met Xaa Asn Arg Phe Ala Thr Ala Phe Val Xaa
      -20                      -15                      -10
GCT TGT GTG CTT AGC CTC ATT TCC ACC ATC TAC ATG GCA GCC TCC ATT      158
Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile
      -5                      1                      5
GGC ACA GAC TTC TGG TAT GAA TAT CGA AGT CCA GTT CAA GAA AAT TCC      206
Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser
      10                      15                      20
AGT GAT TTG AAT AAA AGC ATC TGG GAT GAA TTG                          239
Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Leu
      25                      30
```

## (2) INFORMATION FOR SEQ ID NO: 254:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(43..130)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 176..263  
id C01485



est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(137..219)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 88..170  
id C01485  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 421..459
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq MSLTSGFLRVSQG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

```

CACCAATGTT ATGAATGGCG TGGCCTCCTA CTGCCGTCCC TGTGCCCTAG AAGCCTCTGA    60
TGTGGGCTCC TCCTGCACCT CTTGTCCTGC TGGTTACTAT ATTGACCGAG ATTCAGGAAC   120
CTGCCAMTCC BTGCCCCCCT AACACAATTC TGAAAGCCCA CCAGCCTTAT GGTGTCCAGG   180
CCTGTGTGCC CTGTGGTCCA GGGACCAAGA ACAACAAGAT CCACTCTCTG TGCTACAATG   240
ATTGCACCTT CTCACGCAAC ACTCCAACCA GGACTTTCAA CTACAACTTC TCCGCTTTGG   300
CAAACACCGT CACTCTTGCT GGAGGGCCAA GCTTCACTTC CAAAGGGTTG AAATACTTCC   360
ATCACTTTAC CCTCAGTCTC TGTGAAACC AGGGTAGGAA AATGTCTGTG TGCACCGACA   420
ATG TCA CTG ACC TCC GGA TTC CTG AGG GTG AGT CAG GGT TCT CCA AAT    468
Met Ser Leu Thr Ser Gly Phe Leu Arg Val Ser Gln Gly Ser Pro Asn
      -10                      -5                      1

CTA TCA CAG                                477
Leu Ser Gln
      5 -

```

## (2) INFORMATION FOR SEQ ID NO: 255:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 55..316  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 1..262  
                           id H87671  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 102..261  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 50..209  
                           id N47067  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 55..104  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 2..51  
                           id N47067  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 251..316  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 14..79  
                           id AA135001  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 58..246  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.6  
                           seq AIRTLFSVTGILA/EQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

|   |     |
|---|-----|
| AACTTGCGCGC GCGGCSSGGC TGCAGACGGC TCGAGGGCGC TGGGCACAGG TGTCCTG | 57  |
| ATG GCA AAT TTC AAG GGC CAC GCG CTT CCA GGG AGT TTC TTC CTG ATC | 105 |
| Met Ala Asn Phe Lys Gly His Ala Leu Pro Gly Ser Phe Phe Leu Ile |     |
| -60 -55 -50   |     |
| ATT GGG CTG TGT TGG TCA GTG AAG TAC CCG CTG AAG TAC TTT AGC CAC | 153 |
| Ile Gly Leu Cys Trp Ser Val Lys Tyr Pro Leu Lys Tyr Phe Ser His |     |
| -45 -40 -35   |     |
| ACG CGG AAG AAC AGC CCA CTA CAT TAC TAT CAG CGT CTC GAG ATC GTC | 201 |
| Thr Arg Lys Asn Ser Pro Leu His Tyr Tyr Gln Arg Leu Glu Ile Val |     |
| -30 -25 -20   |     |
| GAA GCC GCA ATT AGG ACT TTG TTT TCC GTC ACT GGG ATC CTG GCA GAG | 249 |
| Glu Ala Ala Ile Arg Thr Leu Phe Ser Val Thr Gly Ile Leu Ala Glu |     |
| -15 -10 -5 1  |     |

CAG TTT GTT CCG GAT GGG CCC CAC CTG CAC CTC TAC CAT GAG AAC CAC 297  
Gln Phe Val Pro Asp Gly Pro His Leu His Leu Tyr His Glu Asn His  
5 10 15

TGG ATA AAG TTA ATG AAT 315  
Trp Ile Lys Leu Met Asn  
20

## (2) INFORMATION FOR SEQ ID NO: 256:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 84..400  
id N34255  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..84  
id N34255  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..304
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 83..298  
id H79944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..54
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 2..48  
id H79944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 336..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 332..378  
id H79944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 304..340
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 299..335  
id H79944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 49..83  
id H79944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 109..298
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 106..295  
id H73369  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..87  
id H73369  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 336..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 336..382  
id H73369  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 295..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 293..324  
id H73369

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 164..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 142..215  
id AA132425  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 327..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 307..375  
id AA132425  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 3..70  
id AA132425  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..163
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 103..142  
id AA132425  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 109..298
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 24..213  
id R97376  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 296..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 212..321  
id R97376  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 187..342
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5

seq AGLLFGSLAGLGA/YQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

```

AGCAGGCACA ACAGAGCCGC TCCCCWCTCC TCGCCCCGCC ACCGGGACGG AGAGCGCCCG      60
CCGCTGCATT TCCGGCGACA CCTCGCAGGT CATTCCTGCG GCTTGC GCGC CTTGTAGAC      120
AGCCGGGGGCC TTCGTSAGAC CGGTGCAGGC CTGGGGTAGT CTCCTGTCTG GACAGAGAAG      180
AGAAAA ATG CAG GAC ACT GGC TCA GTA GTG CCT TTG CAT TGG TTT GGC      228
      Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly
            -50                      -45                      -40

TTT GGC TAC GCA GCA CTG GTT GCT TCT GGT GGG ATC ATT GGC TAT GTA      276
Phe Gly Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val
            -35                      -30                      -25

AAA GCA GGC AGC GTG CCG TCC CTG GCT GCA GGG CTG CTC TTT GGC AGT      324
Lys Ala Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser
            -20                      -15                      -10

CTA GCC GGC CTG GGT GCT TAC CAG CTG TCT CAG GAT CCA AGG AAC GTT      372
Leu Ala Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val
            -5                      1                      5                      10

TGG GTT TTC CTA GCT ACA TCT GGT ACC TTG GCT      405
Trp Val Phe Leu Ala Thr Ser Gly Thr Leu Ala
            15                      20

```

(2) INFORMATION FOR SEQ ID NO: 257:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 119..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 116..234  
id HSC2TH021  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 24..94  
id HSC2TH021  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 238..289  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 234..285  
id HSC2TH021  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 280..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 277..316  
id HSC2TH021  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 130..237  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 23..130  
id R59681  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 238..289  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 130..181  
id R59681  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 280..325  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 173..218  
id R59681  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 183..287  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.4  
seq CCALLTSLXCIWG/PA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

ACCTTCTGTT ACTGTCCGGG GCTGCGGGGC TTGCTTCCKG CGTCAWGGCT CAAAGGGCCT 60

```

TCCCGMATCC TTATGCTGAT TATAACAAAT CCCTGDRCCG AAGSTACTTT GATGCTGCCG 120
GGARGCTGAC TCCTGAGTTC TCACAACGCT TGACCAATAA GATTCGGGAG CTTCTTCAGC 180
AA ATG GAG AKA GGC CTG AAA TCA GCA GAC CCT CGG GAT GGC ACC GGT 227
   Met Glu Xaa Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly
   -35                -30                -25
TAC ACT GRC TTN NKC ARG TAT TGC TGT GCT TTA CTT ACA TCT TTA TGR 275
Tyr Thr Xaa Xaa Xaa Xaa Tyr Cys Cys Ala Leu Leu Thr Ser Leu Xaa
-20                -15                -10                -5
TGT ATT TGG GGA CCT GCC TAC CTA CAG TTA GCA CAT GGC TAT GTA AAG 323
Cys Ile Trp Gly Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys
                1                5                10

```

## (2) INFORMATION FOR SEQ ID NO: 258:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 12..252  
id H64050  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..241  
id R17172  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 2..242  
id HSC15C081  
est

## (ix) FEATURE:

- (A) NAME/KEY: other



(B) LOCATION: 8..241  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..234  
id AA149663  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 29..241  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 29..241  
id HSU46380  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 10..135  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.4  
seq ITGVILLAVGIWG/KV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

|   |     |
|---|-----|
| GGGCTAGTC ATG GCG TCC CCG TCT CGG AGA CTG CAG ACT AAA CCA GTC ATT | 51  |
| Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile           |     |
| -40 -35 -30   |     |
| ACT TGT TTC AAG AGC GTT CTG CTA ATC TAC ACT TTT ATT TTC TGG ATC   | 99  |
| Thr Cys Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile   |     |
| -25 -20 -15   |     |
| ACT GGC GTT ATC CTT CTT GCA GTT GGC ATT TGG GGC AAG GTG AGC CTG   | 147 |
| Thr Gly Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu   |     |
| -10 -5 1  |     |
| GAG AAT TAC TTT TCT CTT TTA AAT GAG AAG GCC ACC AAT GTC CCC TTC   | 195 |
| Glu Asn Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe   |     |
| 5 10 15 20  |     |
| GTG CTC ATT GCT ACT GGT ACC GTC ATT ATT CTT TTG GGC ACC TTG       | 240 |
| Val Leu Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Leu       |     |
| 25 30 35  |     |

## (2) INFORMATION FOR SEQ ID NO: 259:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 385 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..349
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 6..347  
id AA075824  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 344..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 341..382  
id AA075824  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 2..346  
id R55598  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..315  
id HSC33B061  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 156..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 91..320  
id T65515  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..141
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 5..76  
id T65515  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..305
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 2..278

id HSCZRF061  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 119..319
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq LSVSLLPCAGAWS/LL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

```

AAAAGCGGAG MYAGGMNGGG TGAGGAGAGT CGAGGGAGGT GACGCGCGCT GCCGGGGCGA    60
GTTTGCAGAGG GCGGGTGTG AAGAATGTGT GGGCGAACAT CCTGTCACTT ACCTAGAG    118
ATG TTC TCA CGA GAG CTT GCG CCT ACC AGG ATC GGC GGG GCC AGC AGC    166
Met Phe Ser Arg Glu Leu Ala Pro Thr Arg Ile Gly Gly Ala Ser Ser
   -65                      -60                      -55
GGC TCC CGG AGT GGA GGG ACC CTG ATA AGT ACT GCC CCT CTT ACA ACA    214
Gly Ser Arg Ser Gly Gly Thr Leu Ile Ser Thr Ala Pro Leu Thr Thr
   -50                      -45                      -40
AGA GTC CTC AAT CCA ACA GCC CAG TGC TTC TGT CTC GAC TGC ACT TTG    262
Arg Val Leu Asn Pro Thr Ala Gln Cys Phe Cys Leu Asp Cys Thr Leu
  -35                      -30                      -25                      -20
AGA AGG ATG CAG ACT CAT CTG AGC GTA TCA TTG CTC CCA TGC GCT GGG    310
Arg Arg Met Gln Thr His Leu Ser Val Ser Leu Leu Pro Cys Ala Gly
      -15                      -10                      -5
GCT TGG TCC CTT CTT RGT TCA AAG AAA GTG ATC CTT CCA AGC TGC AGT    358
Ala Trp Ser Leu Leu Xaa Ser Lys Lys Val Ile Leu Pro Ser Cys Ser
      1                      5                      10
TCA ATA CTA MCA ACT GTC GTA GTG ATA    385
Ser Ile Leu Xaa Thr Val Val Val Ile
   15                      20

```

## (2) INFORMATION FOR SEQ ID NO: 260:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..128
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 19..104  
id R49759  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 132..194  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 106..168  
id R49759  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 225..311  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.1  
seq LMLGVTL PNSYW/RV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

|   |                 |
|---|-----------------|
| ATTCCTCTGA CCTGCCAGGA AGCAGAGAGA CCCACAGAGC AGGCAGGGAG GCAGAAAGTG | 60              |
| GAGACGGACC TGAGCCCGAG GAAGAGGCAG GCAGAGGCTG AGGCTGATTC CACCCCAGCC | 120             |
| TGCCTGGRAC AAACCCTCCT TAGCCGCAGC CCCTTCCAGT TCCCTAGGGG TTCTGCCCCT | 180             |
| CCCCCTCTCT GGGGCACCAG CCCCCCAGGG TCCTGCATCC NACC ATG TCG ATG GCT  | 236             |
|   | Met Ser Met Ala |
| GTG GAA ACC TTT GGC TTC TTC ATG GCA ACT GTG GGG CTG CTG ATG CTG   | 284             |
| Val Glu Thr Phe Gly Phe Phe Met Ala Thr Val Gly Leu Leu Met Leu   |                 |
| -25 -20 -15 -10   |                 |
| GGG GTG ACT CTG CCA AAC AGC TAC TGG CGA GTG TCC ACT GTG CAC GGG   | 332             |
| Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg Val Ser Thr Val His Gly   |                 |
| -5 1 5  |                 |
| AAC GTC ATC AHC ACC AAC AHC ATC TTC GAG AAC CTC TGG TTT AGC AGT   | 380             |
| Asn Val Ile Xaa Thr Asn Xaa Ile Phe Glu Asn Leu Trp Phe Ser Ser   |                 |
| 10 15 20  |                 |
| GCC GGG   | 386             |
| Ala Gly   |                 |
| 25  |                 |

## (2) INFORMATION FOR SEQ ID NO: 261:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 112..216  
id T86663  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..156
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 120..158  
id AA055880  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 55..114
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq XFLXLXXLSXXWP/XD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```

ACTCAGAAGC TTGGACCGCA TCCTAGCCGC CGACTCACAC AAGGCAGABT TGCC ATG      57
                                     Met
                                     -20

GAG AAA ATT CCA GTG TCA SCA TTC TTG CDC CTN GYG GSC CTC TCK WAS      105
Glu Lys Ile Pro Val Ser Xaa Phe Leu Xaa Leu Xaa Xaa Leu Ser Xaa
      -15                      -10                      -5

AKC TGG CCA SSG GAT ACC ACA GTC AAA CCT GGA GCC AMA AAG GAC ACA      153
Xaa Trp Pro Xaa Asp Thr Thr Val Lys Pro Gly Ala Xaa Lys Asp Thr
      1                      5                      10

AAG GAC TCT CGA SCC AAA CTG CCC CAG ACC CTC TCC AGA GGT TGG GGT      201
Lys Asp Ser Arg Xaa Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp Gly
      15                      20                      25

GAC CAA CTC ATC TGG ACA CGG      222
Asp Gln Leu Ile Trp Thr Arg
      30                      35

```

## (2) INFORMATION FOR SEQ ID NO: 262:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 207..326

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 85..204  
id W69716  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 122..208

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 1..87  
id W69716  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 316..366

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94  
region 195..245  
id W69716  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 282..366

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 94..178  
id W73842  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 207..287

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 17..97  
id W73842  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 257..326

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94  
region 42..111  
id W58108  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 317..366  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
                           region 101..150  
                           id W58108  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 112..312  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5  
                           seq LILERPLVPSAEA/SG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```

ATAAGGCCTC AGGGTCCTGT TTTCCCTGGC CTCTTCTAGA GGGCCCGTGG AMCAGGTCGC      60
AGTGCCTGCT TATTTGGAAA CCAGGTGTGT GAGCCGAATG CCTGCCAGGC C ATG CAC      117
                                   Met His

TCA GCA GAG GAG CCC TTG TAN CTG GCT GCC CTG AGA GGA GCA AGA GGC      165
Ser Ala Glu Glu Pro Leu Xaa Leu Ala Ala Leu Arg Gly Ala Arg Gly
-65                      -60                      -55                      -50

CAC CTC CCA TGT GGC TCT AGA CAC CAC GTG GGC TCA TTA GCC CCA GCG      213
His Leu Pro Cys Gly Ser Arg His His Val Gly Ser Leu Ala Pro Ala
-45                      -40                      -35

TCT GTG CCG GCT CCA GGT GCC TGC CTC TGG GTG TGT GAG TGG GAG ACT      261
Ser Val Pro Ala Pro Gly Ala Cys Leu Trp Val Cys Glu Trp Glu Thr
-30                      -25                      -20

TTG CTC CCT GGC CTC ATC CTA GAG AGG CCC CTG GTG CCT AGT GCT GAG      309
Leu Leu Pro Gly Leu Ile Leu Glu Arg Pro Leu Val Pro Ser Ala Glu
-15                      -10                      -5

GCC TCT GGG GCT GGA AAG CTC AGC AGA AAG GAG GCA CTA CTG AGC AAC      357
Ala Ser Gly Ala Gly Lys Leu Ser Arg Lys Glu Ala Leu Leu Ser Asn
   1                      5                      10                      15

TAT GCA TTG      366
Tyr Ala Leu

```

## (2) INFORMATION FOR SEQ ID NO: 263:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 121..264  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 127..270  
id N24991  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 3..124  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 10..131  
id N24991  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 161..292  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 15..146  
id HSC1WG111  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 176..310  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..135  
id AA001396  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 176..265  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..90  
id AA017578  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 191..265  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..75  
id R17530  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 167..295  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.9



seq GLWLALVDGLVRX/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```
ACTTTTTCCT ACGCAGCCGC TCCTGCCGCC GTGGTCGCTG GAGCTTTGCC TCTCTAGGCC      60
GGCAGCGCCT CTCCTCCATG GTCCTGTCTG TCAGCGCTGT TTTGGGAGCC CGCCGGTGAG    120
GCCGGGCCAC GCTCAGACAC TTCGATCGTC GAGTCTGTCA CTGGGC ATG GCG GGT      175
                                   Met Ala Gly
CAG TTC CGC AGC TAC GTG TGG GAC CCG CTG CTG ATC CTG TCG CAG ATC      223
Gln Phe Arg Ser Tyr Val Trp Asp Pro Leu Leu Ile Leu Ser Gln Ile
-40                               -35                               -25

GTC CTC ATG CAG ACC GTG TAT TAC GGC TCG CTG GGC CTG TGG CTG GCG      271
Val Leu Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala
                               -20                               -15                               -10

CTG GTG GAC GGG CTA GTG CGA ASA GCC CCT CGC TGG ATC SCA GGG          316
Leu Val Asp Gly Leu Val Arg Xaa Ala Pro Arg Trp Ile Xaa Gly
                               -5                               1                               5
```

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 76..316  
id W03477  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..78
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 7..83  
id W03477  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..328

- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 69..325  
id W40364  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..78
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..76  
id W40364  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 164..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 172..336  
id R71313  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 80..166  
id R71313  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..78
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 16..87  
id R71313  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 164..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 151..315  
id H87810  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 59..145  
id H87810  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 14..78  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 2..66  
                           id H87810  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 72..274  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 52..254  
                           id AA135694  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 20..78  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 1..59  
                           id AA135694  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 270..328  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 249..307  
                           id AA135694  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 62..295  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.9  
                           seq VGAVFGLTTCISA/HV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

```

AGGCTGCCCT TGCCTTCCC GAGCTGGCGG GGTCCGTGGT GCGGGATCGA GATTGCGGGC   60
T ATG GCG CCG AAG GTT TTT CGT CAG TAC TGG GAT ATC CCC GAT GGC ACC   109
  Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr
    -75                               -70                               -65

GAT TGC CAC CGC AAA GCC TAC AGC ACC ACC AGT ATT GCC AGC GTC GCT   157
Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala
    -60                               -55                               -50

GGC CTG ACC GCC GCT GCC TAC AGA GTC ACA CTC AAT CCT CCG GGC ACC   205
Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
    -45                               -40                               -35

TTC CTT GAA GGA GTG GCT AAG GTT GGA CAA TAC ACG TTC ACT GCA GCT   253
Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala

```

| -30   | -25 | -20 | -15 |     |
|---|-----|-----|-----|-----|
| GCT GTC GGG GCC GTG TTT GGC CTC ACC ACC TGC ATC AGC GCC CAT GTC |     |     |     | 301 |
| Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val |     |     |     |     |
|   | -10 | -5  | 1   |     |
| CGC GAG AAG CCC GAC GAC CCC CTG AAC CGG                         |     |     |     | 331 |
| Arg Glu Lys Pro Asp Asp Pro Leu Asn Arg                         |     |     |     |     |
|   | 5   | 10  |     |     |

## (2) INFORMATION FOR SEQ ID NO: 265:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(44..183)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..140  
id N78549  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..34)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 150..182  
id N78549  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(103..214)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 100..211  
id N27605  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 150..203
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq WLQVLPVILLLLG/VP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```

AGAGAGAGGG GCCGCTACGC CGCACAGCAA ACAAGCTCCG CGACGTTTCC AGGACCCGGA      60
TAATCCCGCC CTTAGAGCAG AGCCGGAAGA AGGCGGGACG AACCGGAAGA GGGTGAAATG    120
CTTTCGGTAG GCACTCCACG GCTGTGAAG ATG GCG GCG GCT GCG TGG CTT CAG      173
                               Met Ala Ala Ala Ala Trp Leu Gln
                               -15

GTG TTG CCT GTC ATT CTT CTG CTT CTG GGA GTC CCC CCG TCG                215
Val Leu Pro Val Ile Leu Leu Leu Leu Gly Val Pro Pro Ser
-10                               -5                               1

```

## (2) INFORMATION FOR SEQ ID NO: 266:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 59..182  
id AA045287  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 45..168  
id R77973  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 70..193  
id AA136043  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 60..183  
id AA115201  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(1..124)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 60..183  
id R72616  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 5..115  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.8  
seq LLILDMNVLYTDA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

|  |     |
|--|-----|
| ATAG ATG GAA ATA TAC TTT ATA TTT TGT ATC ATC GTG CCT ATA GCC GCT | 49  |
| Met Glu Ile Tyr Phe Ile Phe Cys Ile Ile Val Pro Ile Ala Ala      |     |
| -35 -30 -25  |     |
| GCC ACC GTG TAT AAA TCC TGG TGT CTG CTC CTT ATC CTG GAC ATG AAT  | 97  |
| Ala Thr Val Tyr Lys Ser Trp Cys Leu Leu Leu Ile Leu Asp Met Asn  |     |
| -20 -15 -10  |     |
| GTA TTG TAC ACT GAC GCG TCC CCA CTC GGG                          | 127 |
| Val Leu Tyr Thr Asp Ala Ser Pro Leu Gly                          |     |
| -5 1   |     |

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 48..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 36..128  
id AA054941  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 117..184  
id AA054941  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 48..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 36..206  
id W68324  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 48..141
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 22..115  
id H72703  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 103..191  
id H72703  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..59
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 4..34  
id H72703  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 48..140
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 16..108  
id AA128297  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 97..185  
id AA128297

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 48..141
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 13..106  
id W25240  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 94..182  
id W25240  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 71..163
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq VLLAIGMFFTAWF/FV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```

ACTGTCGACG TGTTCTTCCG GTGGCGGACG GCGGATTAGC CTTCGCGGGG CAAAATTGRA      60
RCYCDRGGCC ATG AGC AGA TAT ACC AGC CCA GTG AAC CCA GCT GTC TTC      109
      Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala Val Phe
            -30                      -25                      -20

CCC CAT CTG ACC GTG GTG CTT TTG GCC ATT GGC ATG TTC TTC ACC GCC      157
Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr Ala
            -15                      -10                      -5

TGG TTC TTC GTT TAC GAG GTC ACC TCT ACC AAG TAC ACT CGT GAT ATC      205
Trp Phe Phe Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg Asp Ile
            1                      5                      10

TAT AAA GAG CTC CAG
Tyr Lys Glu Leu Gln
15

```

## (2) INFORMATION FOR SEQ ID NO: 268:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:



(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 135..179  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 15..59  
id R68571  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 309..413  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.8  
seq LMLSSSLPLLIWL/KD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

```
AACTTTAGCC TCTGATTGCA GGCCACCACT TCATTTACAT GGGGTGAGCA CCAATGCGTT    60
TTGTTCAATT CTTTGTTCAA AACCCCAAGA ATCTGGACAA CTTGCACTCA AGACCCTCTA    120
CGGGTTTGGC GAGCCAGTCC TTCAGTGGCT GTTTTCTAGT AGCTCCTTGG CAATTGAGGG    180
GAACTGGCTG GGACCACTCT CCAGTGCTGT CTGAAGGCCA AGGAGTGAAC AGGGATGGCT    240
GCCCTGCCTT GAAGAGGGAA GGA CTCTTTT CTATCCTTTC CAGCTATAGT CCCTGATCCC    300
TACATGTG ATG CGG TTG GCA GCG GAA GCT CAT CCT GGG CGA ACT CAC ACA    350
      Met Arg Leu Ala Ala Glu Ala His Pro Gly Arg Thr His Thr
      -35                -30                -25

CTT TTC AGG AGA CTT AAA CCT TTT CTT ATG CTA AGT TCT TCC CTT CCC    398
Leu Phe Arg Arg Leu Lys Pro Phe Leu Met Leu Ser Ser Ser Leu Pro
      -20                -15                -10

CTA CTC ATC TGG CTA AAG GAC AGA    422
Leu Leu Ile Trp Leu Lys Asp Arg
      -5                1
```

## (2) INFORMATION FOR SEQ ID NO: 269:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 17..276  
id N23506  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..220  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 8..226  
id R74310  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 219..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 226..268  
id R74310  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 103..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 125..283  
id N42319  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 103..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 119..277  
id N33735  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 105..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 143..299  
id R23867  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 97..213  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.8  
seq IILFSAIVGFIYG/YV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```

AAGTGCCRRA CCTTAGCCCT CACGGTCCTT AAGTCTCGGT CGCCCTCGCC TCKCAGCCTG      60
CCVBCCGCGC TCRKCTGSSC GACTCCTCAG SCAGCC ATG CTG GAG CAT CTG RGC      114
                               Met Leu Glu His Leu Xaa
                               -35
TCG CTG CCC ACG CAG ATG GAT TAC AAG GGC CAG AAG CTA GCT GRR CAG      162
Ser Leu Pro Thr Gln Met Asp Tyr Lys Gly Gln Lys Leu Ala Xaa Gln
                               -30                -25                -20
ATG TTT CAG GGR ATT ATT CTT TTT TCT GCA ATA GTT GGA TTT ATC TAC      210
Met Phe Gln Gly Ile Ile Leu Phe Ser Ala Ile Val Gly Phe Ile Tyr
                               -15                -10                -5
GGG TAC GTG GCT GAA CAG TTC GGG TGG ACT GTC TAT ATA GTT ATG GCC      258
Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr Val Tyr Ile Val Met Ala
      1                5                10                15

GGA
Gly
                                           261

```

## (2) INFORMATION FOR SEQ ID NO: 270:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(154..354)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 70..270  
id AA164185  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..111
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 298..381  
id AA164184  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 297..344
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.8  
seq SKVLFCSFSNVLG/FD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

```

CCAACGTGTG CTTTGAAAAA AAGAAGGGAT GTTTCTGTG TCAAATGAAG GTAATCATAG   60
ATCAAATTTG CTTATTGTCT TGTTCAAATC CTAGAAAACC ATTAGCATTT TTCTTTGCTT   120
GTAATATKAG AATCTAACAC TCATACAGAA TATTGGAAAG GTTACCCTAC AATTGTAAAT   180
TTGAAATTCT CCTTCTAATT CTGTCAGTTA TTTATTGACA TAGTAGTGGT TCTGTAGTCA   240
AGTGCATATA AGGTTTTGAA TGTTACATCT TATTNNNGGA TTWTTATTTT ATCATT  ATG   299
                                         Met
GAG TAT AGC AAA GTT CTA TTT TGT TCT TTT TCA AAT GTA CTT GGT TTT   347
Glu Tyr Ser Lys Val Leu Phe Cys Ser Phe Ser Asn Val Leu Gly Phe
-15          -10          -5          1
GAT TAT                                         353
Asp Tyr

```

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 225 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Prostate

(ix) FEATURE:  
 - (A) NAME/KEY: other  
 (B) LOCATION: 19..133  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 1..115  
                           id HSC13B041  
                           est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 124..226  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 105..207  
                           id HSC13B041  
                           est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 124..226

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 71..173  
id T08849  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 53..133  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..81  
id T08849  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 53..135  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..83  
id H88132  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 124..192  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 71..139  
id H88132  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 192..226  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 140..174  
id H88132  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 53..144  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..92  
id T33149  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 145..226  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 92..173  
id T33149  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..133
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..82  
id AA121114  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 192..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 141..175  
id AA121114  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 46..123
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq LIMQLGSVLLTRC/PF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```

ACTCTCTGAC TGGGGTGAGG CCGCAGCGGA CTGCCCTTTC CCAAG ATG GCG TCG AAG      57
                                   Met Ala Ser Lys
                                   -25

ATA GGT TCG AGA CGG TGG ATG TTG CAG CTG ATC ATG CAG TTG GGT TCG      105
Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met Gln Leu Gly Ser
-20                               -15                               -10

GTG CTG CTC ACA CGC TGC CCC TTT TGG GGC TGC TTC AGC CAG CTC ATG      153
Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe Ser Gln Leu Met
-5                               1                               5                               10

CTG TAC GCT GAG AGG GCT GAG GCA CGC CGG AAG CCC GAC ATC CCA GTG      201
Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro Asp Ile Pro Val
-                               15                               20                               25

CCT TAC CTG TAT TTC GAC AGT GGG      225
Pro Tyr Leu Tyr Phe Asp Ser Gly
30

```

## (2) INFORMATION FOR SEQ ID NO: 272:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..287
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 9..294  
id W52125  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..283
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..265  
id AA024623  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..284
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..263  
id H55824  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 2..288  
id R62921  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..287
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 57..242  
id N31702  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..100
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..56  
id N31702  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 69..224
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7

seq LGLALGRLEGGSA/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```

ATTGGCTCCG GATCGTGCCT GAGGCGGCTT CGTGGGCAGC GAGAGTCACA GACAAGACAG   60
CAAGCAGG ATG GAG CAC TAC CGG AAA GCT GGC TCT GTA GAG CTC CCA GCG   110
      Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala
            -50                -45                -40

CCT TCC CCA ATG CCC CAG CTA CCT CCT GAT ACC CTT GAG ATG CGG GTC   158
Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val
            -35                -30                -25

CGA GAT GGC AGC AAA ATT CGC AAC CTG CTG GGG TTG GCT CTG GGT CGG   206
Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg
            -20                -15                -10

TTG GAG GGC GGC AGT GCT CGG CAT GTA GTG TTC TCA GGT TCT GGC AGG   254
Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg
            -5                1                5                10

GCT GCA GGA AAG GCT GTC AGC TGC GCT GAG ATT GTC AAG CGG CGG GTC   302
Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val
            15                20                25

CCG   305
Pro

```

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 2..213  
id W26501  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 6..219



id W28013  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(211..324)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 334..447  
id W28077  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 215..324  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..110  
id HSC3LG011  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 104..181  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.6  
seq LIALTCLDGTTVS/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

```

AGCATTTTGC AAAGATGGCT GTAGGAATGG AGGAGCCTGT ATTGCCGCTA ATGTGTGTGC      60
CTGCCCACAA GGCTTCACTG GACCCAGCTG TGAAACGACA TTG ATG AAT GCT CTG      115
                               Met Asn Ala Leu
                               -25

ATG GTT TTG TTC AAT GTG ACA GTC GTG CTA ATT GCA TTA ACC TGC CTG      163
Met Val Leu Phe Asn Val Thr Val Val Leu Ile Ala Leu Thr Cys Leu
-20                      -15                      -10

GAT GGT AEC ACT GTG AGT GCA GAG ATG GCT ACC ATG ACA ATG GGA TGT      211
Asp Gly Thr Thr Val Ser Ala Glu Met Ala Thr Met Thr Met Gly Cys
-5                      1                      5                      10

TTT CAC CAA GTG GAG AAT CGT GTG AAG ATA TTG ATG AGT GTG GGA CCG      259
Phe His Gln Val Glu Asn Arg Val Lys Ile Leu Met Ser Val Gly Pro
15                      20                      25

GGA GGC ACA GCT GTG CCA ATG ATA CCA TTT GCT TCA ATT TGG ATG GCG      307
Gly Gly Thr Ala Val Pro Met Ile Pro Phe Ala Ser Ile Trp Met Ala
30                      35                      40

GAT ATG ATT GNC GAT      322
Asp Met Ile Xaa Asp
45

```

## (2) INFORMATION FOR SEQ ID NO: 274:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 337 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 94..339  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 62..307  
                           id AA133635  
                           est
- (ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 32..97  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 1..66  
                           id AA133635  
                           est
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 191..325  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.6  
                           seq VLVYLVTAERVWS/DD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

```

ACTCCCAGGC TGGGCCAGCA CACCCGGCAG GCTCTGTCCT GGAAACAGGC TTCAACGGGC   60
TTCCCCGAAA ACCTTCCCCG CTTCTGGRTA TGAAVWTKCA AGCTGCTTGC TGAGTCCTAT   120
TGCCGGCTGC TGGGAGCMAG GAGAGCCCTG AGGAGTAGTC ACTCAGTAGC AGCTGACGCG   180
TGGGTCCACC ATG AAC TGG AGT ATC TTT GAG GGA CTC CTG AGT GGG GTC   229
      Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val
      -45                      -40                      -35

AAC AAG TAC TCC ACA GCC TTT GGG CGC ATC TGG CTG TCT CTG GTC TTC   277
Asn Lys Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe
      -30                      -25                      -20

ATC TTC CGC GTG CTG GTG TAC CTG GTG ACG GCC GAG CGT GTG TGG AGT   325
Ile Phe Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser
      -15                      -10                      -5

GAT GAC CAC AAG   337
Asp Asp His Lys

```

## (2) INFORMATION FOR SEQ ID NO: 275:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..287
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 37..119  
id T82645  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 129..176
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq SLFIYIFXTCSNT/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

```

ACTGTCCCAT TCCTCCCCCT ACAACACACA CACCTTTCAG GCAGGGASGN GATGAGCTTC   60
CAGCCCCAAG AGTGGAGGCT GCCACATCCT AACATASGKA KCTATTGRRR AGGAAKSAGT  120
GTGTATCT ATG ATT ATA TCT CTG TTC ATC TAT ATA TTT TTK ACA TGT AGC   170
Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Xaa Thr Cys Ser
      -15                      -10                      -5

AAC ACC TCT CCA TCT TAT CAA KGA ACT CAA CTC GGT CTG GGT CTC CCC   218
Asn Thr Ser Pro Ser Tyr Gln Xaa Thr Gln Leu Gly Leu Gly Leu Pro
      1                      5                      10

AGT GCC CAG TGG TGG CCT TTG ACA GGT AGG AGG ATG CAG TGC TGC AGG   266
Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg
      15                      20                      25                      30

CTA TTT TGT TTT KTG TTA CAA   287
Leu Phe Cys Phe Xaa Leu Gln
      35

```

## (2) INFORMATION FOR SEQ ID NO: 276:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..156
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 40..195  
id AA227366  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..156
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 4..159  
id AA069390  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..152
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..144  
id AA248850  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..78  
id AA248912  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 70..114  
id AA248912  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 61..108
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4

seq LNSLSALAEAVG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

```
ATGGCTGTCA GAGGTGGGCG GCTTTGACCG AGAGGCTGCT GGAGCTCGTG TTTGGACGCG      60
ATG TTT CGT CTG AAC TCA CTT TCT GCT TTG GCA GAA CTG GCT GTG GGT      108
Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
   -15                -10                -5

TCT CGA TGG TAC CAT GGA GGA TCA CAG CCC ATC CAG ATC CGG CGG AGA      156
Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Arg Arg
   1                5                10                15
```

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..330
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 69..301  
id R99696  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..98
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..70  
id R99696  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 206..330
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 164..288  
id W90165  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..209

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 55..166  
id W90165  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 43..98  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..56  
id W90165  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 98..330  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 82..314  
id H91200  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 16..98  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..83  
id H91200  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 98..249  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 62..213  
id R06513  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 238..288  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq TLRTWLCCAGSWA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

```
ACATACTTGC AGCTARAAC T AAATATTGCT GCTTGGGGAC CTCCTTCTAG CCTTAAATTT 60
CAGCTCATCA CCTTCACCTG CCTTGGTCAT GGCTCTGSCT ATTCTCCTTG ATCCTTGCCA 120
TTTGCACCAG ACCTGGATTC CTAGCGTCTC VATCTGGAGT GCGGCTGGTG GGGGGCCTCC 180
ACCGCTGTGA AGGGCGGGTG GAGGTGGAAC AGAAAGGCCA GTGGGGCACC GTGTGTG 237
ATG ACG GCT GGG ACA TTA AGG ACG TGG CTG TGT TGT GCC GGG AGC TGG 285
```

Met Thr Ala Gly Thr Leu Arg Thr Trp Leu Cys Cys Ala Gly Ser Trp  
 -15 -10 -5

GCT GTG GAG CTG CCA GCG GAA CCC CTA GTG GTA TTT TGT AWG AGC ACC 333  
 Ala Val Glu Leu Pro Ala Glu Pro Leu Val Val Phe Cys Xaa Ser Thr  
 1 5 10 15

AGC AGA AAA AGA GCA AAA GGT CTC ATC CAA TCA GTC 369  
 Ser Arg Lys Arg Ala Lys Gly Leu Ile Gln Ser Val  
 20 25

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..99)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
 region 99..196  
 id AA088690  
 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(87..187)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
 region 12..112  
 id AA088690  
 est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 111..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
 seq RLLVILCVSVKAG/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

ACTACAGCAT GGCCACGTGG AGGCAGCGGC AGGAGAAAAA GCAGCTGGGC TTCTTCTGAA 60

CCCAAGCCCT CTCGACTGCC CCTATCCCCT GGAVCCCCAA CATACCTACA ATG CTG 116  
 Met Leu

GGG AGG CCC TGC TTC CAC TCC CCT CAG AGG CTT TTG GTC ATC CTC TGC 164

Gly Arg Pro Cys Phe His Ser Pro Gln Arg Leu Leu Val Ile Leu Cys  
-20 -15 -10

GTG TCA GTA AAA GCA GGC AGC ACG  
Val Ser Val Lys Ala Gly Ser Thr  
-5 1

188

## (2) INFORMATION FOR SEQ ID NO: 279:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 106..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 119..274  
id AA280906  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 15..112  
id AA280906  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 260..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 272..303  
id AA280906  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 224..375  
id HUM406F04B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other



- (B) LOCATION: 12..112
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..101  
id HUM406F04B  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 106..140
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 94..128  
id HUM406F04B  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 124..253  
id AA133362  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..92
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..88  
id AA133362  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 260..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 251..282  
id AA133362  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 106..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 94..249  
id N57260  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..92
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..83  
id N57260  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 260..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 247..278  
id N57260  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..234
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 42..235  
id W25567  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..40
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..40  
id W25567  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 194..277
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq LQFVLPVATQIQQ/EV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

```

AGGGGCGTTG GGAACGGTTG TAGGACGTGG CTCTTTATTC GTGAGTTTTC CATTTACCTC    60
CGCTGAACCT AGAGCTTCAG ACGCCCTATG GCGTCCGCCT CGACACCAAC CGGCGGCCTT    120
GAGCGCTGAG CAAGCAAAGG TGGTCCTCGC GGAGGTGATC CAGGCGTTCT CCGCCCCGGA    180
GAATGCAGTG CGC ATG GAC GAG GCT CGG GAT AAC GCC TGC AAC GAC ATG        229
      Met Asp Glu Ala Arg Asp Asn Ala Cys Asn Asp Met
                -25                      -20

GGT AAG ATG CTG CAA TTC GTG CTG CCC GTG GCC ACG CAG ATC CAG CAG        277
Gly Lys Met Leu Gln Phe Val Leu Pro Val Ala Thr Gln Ile Gln Gln
      -15                      -10                      -5

GAG GTT ATC AAA                                                    289
Glu Val Ile Lys
1

```

## (2) INFORMATION FOR SEQ ID NO: 280:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..69
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..32  
id H56508  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 287..349
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq LCALGSAPSSMWA/GE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```

AAACCTCCGT GGCTAGTCTT GACGTGGCGG GTTGCTTTCC AAAATGGCGC GGGTGCTGAA    60
GGCTGCAGCC GCDBAATGCC GTAGGTGAAT ACCGGGCACC GCCGACCTTC GCCATGGGAC   120
AGGGAGCGTG GGAACGGCGG TCGGGGGCGG AGGAKGCCTC GGTGTGGCCA AAGCACCTTG   180
ATCTAATGTC CTCCCCCGGG GGCGCGTTCC ACAGCAGCTG CTGTCACTTW KGGCAGAGGG   240
TGCCTTCCAG AAGCGCCACC GCTTAGTAGC GGGGATTGCB TTGTGC ATG AGT CCC       295
                                   Met Ser Pro
                                   -20

ATT TCE ATC CGA GAG CTG TGC GCC TTG GGC TCT GCA CCT TCC AGT ATG       343
Ile Ser Ile Arg Glu Leu Cys Ala Leu Gly Ser Ala Pro Ser Ser Met
      -15                      -10                      -5

TGG GCB GGA GAG                                                         355
Trp Ala Gly Glu
      1

```

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 2..149  
id AA095592  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..105
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 219..306  
id T70757  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 163..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 37..129  
id H66541  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 163..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 37..129  
id R92835  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 172..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 14..97  
id H87601  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 52..90
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq MTDLLSASPWALT/IV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

ACCAAGTTTG AGCACCTGGA AAGGGTTTAT GCTGACATCC CCTTTCTGTT G ATG ACG  
Met Thr

|   |     |
|---|-----|
| GAC CTC TTA AGT GCC TCA CCC TGG GCC CTC ACT ATT GTT TCC AGT GAG | 105 |
| Asp Leu Leu Ser Ala Ser Pro Trp Ala Leu Thr Ile Val Ser Ser Glu |     |
| -10 -5 1 5  |     |
| CTC CAC CTT GCT CCA TCC ATG ACC ACA GTG GAC CAG CTC GAG TCT CAA | 153 |
| Leu His Leu Ala Pro Ser Met Thr Thr Val Asp Gln Leu Glu Ser Gln |     |
| 10 15 20  |     |
| GTG GAC AAT GTK ATC TTA CAG ACT GGA GAG AGT GCT AGT GAA TGC TTT | 201 |
| Val Asp Asn Val Ile Leu Gln Thr Gly Glu Ser Ala Ser Glu Cys Phe |     |
| 25 30 35  |     |
| TGT CTT CAA TGC CCA TCT CTT GGA AAT ATT GAA GGT GGA GTA GCA ACC | 249 |
| Cys Leu Gln Cys Pro Ser Leu Gly Asn Ile Glu Gly Gly Val Ala Thr |     |
| 40 45 50  |     |
| GGG CAY HGG   | 258 |
| Gly His Xaa   |     |
| 55  |     |

## (2) INFORMATION FOR SEQ ID NO: 282:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 10..206  
id AA074428  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 196..257  
id AA074428  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..175

id AA158941  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 193..285  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 165..257  
id AA158941  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 37..202  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..166  
id AA148039  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 193..254  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 156..217  
id AA148039  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 250..285  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 214..249  
id AA148039  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 74..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..207  
id H72224  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 76..153  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.2  
seq LTCGPALVPRLWA/TC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

AAGAGGCTAG AAGCTGGATT CAGCGTGTCC GCGACCTCAC CTTTAGGTCC TGTGAGGGAC 60

GGCCCAGGTG GCAGG ATG TCC TGG TCT GGC CTT CTC CAT GGC CTC AAC ACG 111

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..93
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 1..45  
id AA003782  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 25..93
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq LEAFSQAISAIQA/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

```

AAKAGCTGCT GTGGCGGCGG CAAC ATG GCG GAC GTG ATA AAT GTC AGT GTG      51
                        Met Ala Asp Val Ile Asn Val Ser Val
                        -20                               -15

AAC CTG GAG GCC TTT TCC CAG GCC ATT AGT GCC ATC CAG GCG CTG CGA      99
Asn Leu Glu Ala Phe Ser Gln Ala Ile Ser Ala Ile Gln Ala Leu Arg
                        -10                               -5                               1

TCC AGC GTG AGC AGG GTG TTC GAC TGC CTG AAG GAT GGG ATG CGG AAC      147
Ser Ser Val Ser Arg Val Phe Asp Cys Leu Lys Asp Gly Met Arg Asn
                        5                               10                               15

AAG GAG ACG CTG GAG GGC CGG GAG AAG GCC TTT ATT GCG CAC TTC CAG      195
Lys Glu Thr Leu Glu Gly Arg Glu Lys Ala Phe Ile Ala His Phe Gln
                        20                               25                               30

GAC AAC TTA CAT TCG GTC AAC CGG GAC CCA                                225
Asp Asn Leu His Ser Val Asn Arg Asp Pro
                        35                               40

```

## (2) INFORMATION FOR SEQ ID NO: 284:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(210..340)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99



region 172..302  
id AA062591  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 109..204
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq RLLSSLLLTMSNN/NP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```

AGACCCGATG GACCCCGGCG ACGCSCCATT TTGGAGTCTT CCCTAAGGAT CCTCTACCGG      60
CTTTTCGAGT CAGTGCTGCC GCCGCTGCCC GCGGCTTTGC AGAGCAGG ATG AAT GTG      117
                                         Met Asn Val
                                         -30

ATA GAC CAC GTG CGG GAC ATG GCG GCC GCG GGG CTG CAC TCC AAC GTG      165
Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu His Ser Asn Val
                    -25                    -20                    -15

CGG CTC CTC AGC AGC TTG TTA CTT ACA ATG AGT AAT AAC AAC CCT GAG      213
Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn Asn Asn Pro Glu
                    -10                    -5                      1

TTA TTC TCC CCA CCT CAG AAG TAC CAG CTT TTG GTG TAT CAT GCA GAT      261
Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val Tyr His Ala Asp
                    5                      10                      15

TCT CTC TTT CAT GAT AAG GAA TAT CGG AAT GCT GTG AGT AAG TAT ACC      309
Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val Ser Lys Tyr Thr
    20                      25                      30                      35

ATG GCT TTA CAG CAG AAG AAA GCG CTA AGT      339
Met Ala Leu Gln Gln Lys Lys Ala Leu Ser
                    40                      45

```

## (2) INFORMATION FOR SEQ ID NO: 285:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..41)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90

region 66..105  
id AA085310  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 70..117
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq ACLAWTAVRPSAC/CH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```
AAAGTGAGTT TGCGAACGGA GCAGCTGCTG CAGCAGGGCC CATGGCGGAC ACCCAGTACA    60
TCCTGCCCCA ATG ACA TCG GCG TGT CTA GCC TGG ACT GCC GTG AGG CCT TCC    111
      Met Thr Ser Ala Cys Leu Ala Trp Thr Ala Val Arg Pro Ser
            -15                      -10                      -5

GCC TGC TGT CAC CCA CAG AGC GCC AAC TGG                                141
Ala Cys Cys His Pro Gln Ser Ala Asn Trp
      1                      5
```

## (2) INFORMATION FOR SEQ ID NO: 286:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(147..290)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 141..284  
id W12393  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 249..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..41  
id HSC2TF111  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 60..224

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4  
seq VFGMSSSSGASNS/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

```

ATCTCAACTT GGACTTGCAA TCACAGAACA TTTACCACCA TGGAAGAGAA GGAAGTAGG      59

ATG AAT GGA AGT AGG ACT CTA ACG CAC AGC ATT AGT GAT GGA CAA CTT      107
Met Asn Gly Ser Arg Thr Leu Thr His Ser Ile Ser Asp Gly Gln Leu
-55                -50                -45                -40

CAA GGT GGC CAG TCC AAT AGT GAA CTA TTT CAG CAG GAG SSA CAG ACA      155
Gln Gly Gly Gln Ser Asn Ser Glu Leu Phe Gln Gln Glu Xaa Gln Thr
                -35                -30                -25

GCA CCA GCT CAA GTT CCT CAA GGC TTT AAT GTT TTT GGA ATG TCC AGT      203
Ala Pro Ala Gln Val Pro Gln Gly Phe Asn Val Phe Gly Met Ser Ser
                -20                -15                -10

TCC TCT GGT GCT TCA AAT TCA GCA CCA CAT CTT GGA TTT CAC TTA GGC      251
Ser Ser Gly Ala Ser Asn Ser Ala Pro His Leu Gly Phe His Leu Gly
                -5                1                5

AGC AAA GGA ACA TCT AGC CTT TCT CAA CAA ACT CCC GGG      290
Ser Lys Gly Thr Ser Ser Leu Ser Gln Gln Thr Pro Gly
10                15                20

```

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(68..194)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 204..330  
id N35493  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(208..323)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 75..190  
id N35493

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..79)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 318..395  
id N35493  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 186..233
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq FFLFLSFVLMYDG/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

```
ATAAAAGAAG CAGCAAATAG AATTTCCCAC AAAGTAAGTT GACTCTAAAT CTTAAGTATT   60
ACCTAGTTTT TTAAAGGTTT GAATATAATA ATGCAGTATT TGCAGTATAA AAAGGAAGGA  120
ATTTGTAGAG AATCATTTTG GTGCTCAAGT CTCTTAGCAG TGCCTTATTG CCTCATAGCA  180
AGAAG ATG CTG GGG TTT TTT TTG TTT TTG TCC TTT GTA TTA ATG TAT GAT  230
Met Leu Gly Phe Phe Leu Phe Leu Ser Phe Val Leu Met Tyr Asp
   -15                      -10                      -5

GGT TTG CGC CTT TTT GGC ATT CTT TCA ACA TGT CGT GTA CAT CAC ACC   278
Gly Leu Arg Leu Phe Gly Ile Leu Ser Thr Cys Arg Val His His Thr
   1                      5                      10                      15

ATG AAT CAG TTC CTA ATT GAT ATA TCT AGC TTT ACC TCC CGA GTT CGG   326
Met Asn Gln Phe Leu Ile Asp Ile Ser Ser Phe Thr Ser Arg Val Arg
          20                      25                      30
```

## (2) INFORMATION FOR SEQ ID NO: 288:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 219..380
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 46..207

id N95583  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 219..335  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 46..162  
id AA283710  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 336..380  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 162..206  
id AA283710  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 240..320  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq SIKVLLQSALSLG/RS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```

AGTGGCTCTT CTGACCCAAG GCCCCGCCGT CCAGGTAGGG GGCTGTGGCC TCTAGGGATC    60
AGGGACTACT TACCTGCGAA TCCCGGTTGC CCGCCGCCA RCACGTCCGK TYCCSTAARG    120
CARAMCGCCT KGGCTCCTGG CTGAACCGTC TTCTCAMCGT TTGSCGGAGT CTGAMCTCCC    180
CACGCTTAGT CCACTAACGR AGCTATCCCT GTCCTGMCC CACAGCTTCT AAGTGCCAG    239
ATG ATG GAG GAG CGT GCC AAC CTG ATG CAC ATG ATG AAA CTC AGC ATC    287
Met Met Glu Glu Arg Ala Asn Leu Met His Met Met Lys Leu Ser Ile
      -25                      -20                      -15

AAG GTG TTG CTC CAG TCG GCT CTG AGC CTG GGC CGC AGC CTG GAT GCG    335
Lys Val Leu Leu Gln Ser Ala Leu Ser Leu Gly Arg Ser Leu Asp Ala
      -10                      -5                      1                      5

GAC CAT GCC CCC TTG CAG CAG TTC TTT GTA GTG ATG GAG CAC TGC TCA    383
Asp His Ala Pro Leu Gln Gln Phe Phe Val Val Met Glu His Cys Ser
              10                      15                      20

```

## (2) INFORMATION FOR SEQ ID NO: 289:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 57..180  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 97  
                            region 15..138  
                            id AA090170  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 226..286  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 98  
                            region 184..244  
                            id AA090170  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 21..242  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 90  
                            region 1..222  
                            id HSU46267  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 143..319  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 90  
                            region 220..396  
                            id AA048294  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 149..286  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 92  
                            region 139..276  
                            id AA118611  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 143..286  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 92  
                            region 88..231  
                            id AA063937  
                            est
- (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 80..130  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
 seq XIVSAALLAFVQT/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

```

AGTTGGTGGG GCTGGGGGAT GAGAGCTGCA CCGCGCGGGA YAAGTCGCCG GCGGCGCCCG      60
AMGGAGCAGA ACAGAGAGC ATG GAG CTG GAG AKG ATC GTC AGT GCA GCC CTC      112
          Met Glu Leu Glu Xaa Ile Val Ser Ala Ala Leu
                    -15                      -10

CTT GCC TTT GTC CAG ACA CAC CTC CCG GAG GCC GAC CTC AGT GGC TTG      160
Leu Ala Phe Val Gln Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu
      -5                      1                      5                      10

GAT GAG GTC ATC TTC TCC TAT GTG CKT GGG GTC CTG GAG GAC CTG GGC      208
Asp Glu Val Ile Phe Ser Tyr Val Xaa Gly Val Leu Glu Asp Leu Gly
          15                      20                      25

CCC TCG GGC CCA TCA GAG GAG AAC TTC GAT ATG GAG GCT TTC ACT GAG      256
Pro Ser Gly Pro Ser Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu
          30                      35                      40

ATG ATG GAG GCC TAK GTG CCT GGC TTC GCC CAC ATC CCC AGG GGM ACA      304
Met Met Glu Ala Xaa Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr
          45                      50                      55

ATA GGG GAS ATG ATG                                          319
Ile Gly Xaa Met Met
      60
  
```

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 2..273  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 8..279  
 id T30552  
 est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 3..273  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 1..271  
                           id C14403  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 2..273  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 14..285  
                           id T30625  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 4..273  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 1..270  
                           id T32136  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 3..270  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 1..268  
                           id C14440  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 98..175  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
                           seq SLIPLXFIGTGA/TG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

AGGAAGTCCG TAGTGTCTCA TTGCRGATAA TTTTGTAGCTT AGGGCCTKGT GGCTAGGKCG      60
GTTCTCTCCK KTCCAGTCGG AGACCTCTGC SGVRRRC ATG CTC CGC CAG ATC ATC      115
                               Met Leu Arg Gln Ile Ile
                               -25

GGT CAG GCC AAG AAG CAT CCG AGC TTG ATC CCC CTC TTT KTA TTT ATT      163
Gly Gln Ala Lys Lys His Pro Ser Leu Ile Pro Leu Phe Xaa Phe Ile
-20                      -15                      -10                      -5

GGR ACT GGA GCT ACT GGA GCA ACA CTG TAT CTC TTG CGT CTG GCA TTG      211
Gly Thr Gly Ala Thr Gly Ala Thr Leu Tyr Leu Leu Arg Leu Ala Leu
                      1                      5                      10

TTC AAT CCA GRT GTT TGT TGG GAC AGA RRT AAC CCA GAG CCC TGG AAC      259
Phe Asn Pro Xaa Val Cys Trp Asp Arg Xaa Asn Pro Glu Pro Trp Asn

```



15

20

25

RRA CTG GGC CCC GAA  
Xaa Leu Gly Pro Glu  
30

274

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 37..330  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq WTSLTCSLVVVDG/CG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

|      |       |       |       |      |         |      |     |     |     |     |     |     |     |     |     |     |
|------|-------|-------|-------|------|---------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AAGT | CGGTG | GAGCC | AGGCG | TGGA | AAGTCGA | CACA | AAG | ATG | GTG | AAG | GAG | ACC | CAG |     | 54  |     |
|      |       |       |       |      |         |      |     | Met | Val | Lys | Glu | Thr | Gln |     |     |     |
|      |       |       |       |      |         |      |     |     |     |     | -95 |     |     |     |     |     |
|      |       |       |       |      |         |      |     |     |     |     |     |     |     |     |     |     |
| TAC  | TAT   | GAC   | ATC   | CTG  | GGC     | GTG  | AAG | CCC | AGC | GCG | TCC | CCG | GAG | AGA | TCA | 102 |
| Tyr  | Tyr   | Asp   | Ile   | Leu  | Gly     | Val  | Lys | Pro | Ser | Ala | Ser | Pro | Glu | Arg | Ser |     |
|      |       | -90   |       |      |         |      | -85 |     |     |     |     | -80 |     |     |     |     |
|      |       |       |       |      |         |      |     |     |     |     |     |     |     |     |     |     |
| AGA  | AGG   | CCT   | ATC   | GGA  | AGC     | TGG  | CGC | TCA | AGT | ACC | ACC | CGG | ACA | AGA | ACC | 150 |
| Arg  | Arg   | Pro   | Ile   | Gly  | Ser     | Trp  | Arg | Ser | Ser | Thr | Thr | Arg | Thr | Arg | Thr |     |
|      | -75   |       |       |      |         | -70  |     |     |     |     | -65 |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CGG | ATG | AGG | GCG | AGA | AGT | TTA | AAC | TCA | TAT | CCC | AGG | CAT | ATG | AAG | TGC | 198 |
| Arg | Met | Arg | Ala | Arg | Ser | Leu | Asn | Ser | Tyr | Pro | Arg | His | Met | Lys | Cys |     |
| -60 |     |     |     |     | -55 |     |     |     |     | -50 |     |     |     |     | -45 |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| TTT | CAG | ATC | CAA | AGA | AAA | GGG | ATG | TTT | ATG | ACC | AAG | GCG | GAG | AGC | AGG | 246 |
| Phe | Gln | Ile | Gln | Arg | Lys | Gly | Met | Phe | Met | Thr | Lys | Ala | Glu | Ser | Arg |     |
|     |     |     | -40 |     |     |     |     | -35 |     |     |     |     | -30 |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| CAA | TBV | AAG | AAG | GAG | GCT | CAG | GCA | GCC | CCA | GCT | TCT | CTT | CAC | CCA | TGG | 294 |
| Gln | Xaa | Lys | Lys | Glu | Ala | Gln | Ala | Ala | Pro | Ala | Ser | Leu | His | Pro | Trp |     |
|     |     | -25 |     |     |     |     | -20 |     |     |     |     | -15 |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| ACA | TCT | TTG | ACA | TGT | TCT | TTG | GTG | GTG | GTG | GAC | GGA | TGC | GGG |     |     | 336 |
| Thr | Ser | Leu | Thr | Cys | Ser | Leu | Val | Val | Val | Asp | Gly | Cys | Gly |     |     |     |
|     |     | -10 |     |     |     | -5  |     |     |     |     |     | 1   |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 292:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..194
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 2..178  
id W25476  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 206..359
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 193..346  
id W25476  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 359..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 347..384  
id W25476  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..278  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 19..276  
id HUM179H07B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 279..379  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 278..378  
id HUM179H07B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 17..175  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 27..185  
id AA002128  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 171..292  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 182..303  
id AA002128  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 358..396  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 373..411  
id AA002128  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 325..358  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 339..372  
id AA002128  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 204..396  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 186..378  
id AA253291  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 22..202  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 5..185  
                           id AA253291  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 42..260  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 26..244  
                           id W45609  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 251..359  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 234..342  
                           id W45609  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 363..396  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 348..381  
                           id W45609  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 59..166  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.8  
                           seq RALSTXLFGSIRG/AA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

|  |     |
|--|-----|
| AGTGCGCAGA CGCAGGGGTC GGC GCCGGGT GAGAGCGTGC GGCCGGATTC ACCACAAC | 58  |
| ATG GCA AAT CTT TTT ATA AGG AAA ATG GTG AAC CCT CTG CTC TAT CTC  | 106 |
| Met Ala Asn Leu Phe Ile Arg Lys Met Val Asn Pro Leu Leu Tyr Leu  |     |
| -35 -30 -25  |     |
| AGT CGT CAC ACG GTG AAG CCT CGA GCC CTC TCC ACA NTT CTA TTT GGA  | 154 |
| Ser Arg His Thr Val Lys Pro Arg Ala Leu Ser Thr Xaa Leu Phe Gly  |     |
| -20 -15 -10 -5   |     |
| TCC ATT CGA GGT GCA GCC CCC GTG GCT GTG GAA CCC GGG GCA GCA GTG  | 202 |
| Ser Ile Arg Gly Ala Ala Pro Val Ala Val Glu Pro Gly Ala Ala Val  |     |
| 1 5 10   |     |

|   |     |
|---|-----|
| CGC TCA CTT CTC TCA CCC GGC CTC CTG CCC CAT CTG CTG CCT GCG CTG | 250 |
| Arg Ser Leu Leu Ser Pro Gly Leu Leu Pro His Leu Leu Pro Ala Leu |     |
| 15 20 25  |     |
| GGG TTC AAA AAC AAG ACT GTC CTT AAG AAG CGC TGC AAG GAC TGT TAC | 298 |
| Gly Phe Lys Asn Lys Thr Val Leu Lys Lys Arg Cys Lys Asp Cys Tyr |     |
| 30 35 40  |     |
| CTG GTG AAG AGG CGG GGT CGG TGG TAC GTC TAC TGT AAA ACC CAT CCG | 346 |
| Leu Val Lys Arg Arg Gly Arg Trp Tyr Val Tyr Cys Lys Thr His Pro |     |
| 45 50 55 60   |     |
| AGG CAC AAG CAG AGA CAC ATG TAN ACC CTT TCC CTC CAG AGT CAC GCA | 394 |
| Arg His Lys Gln Arg His Met Xaa Thr Leu Ser Leu Gln Ser His Ala |     |
| 65 70 75  |     |
| CAA   | 397 |
| Gln   |     |

## (2) INFORMATION FOR SEQ ID NO: 293:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 115..216
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 41..142  
id H64274  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 74..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..43  
id H64274  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 115..216
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 36..137  
id R16956  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..38  
id R16956  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 123..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 57..148  
id W04201  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 4..57  
id W04201  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 123..190
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 50..117  
id N76590  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 2..43  
id N76590  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(107..195)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 323..411  
id N70265  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 106..201
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq RIHLCQRSPGSQG/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

```

ACCCTGCCTC ATGCAGCCTA TGGGCTAGGC TTTAGGGTCC GCGGTTGGTC AKACCGGAGC   60
ACTTGGCCTG AAGACCTGGA ATTGGYGACT TCGATATTAA CAAGG ATG GCG GCG GCC   117
                                     Met Ala Ala Ala
                                     -30

GCA GCA AGT CGA GGA KTC GGG GCA AAG CTG GGC CTG CGT GAN ATT CGC   165
Ala Ala Ser Arg Gly Xaa Gly Ala Lys Leu Gly Leu Arg Xaa Ile Arg
          -25                      -20                      -15

ATC CAC TTA TGT CAG CGC TCG CCC GGC AGC CAG GGC GTC AGG GAC TTC   213
Ile His Leu Cys Gln Arg Ser Pro Gly Ser Gln Gly Val Arg Asp Phe
          -10                      -5                      1

ATT                                     216
Ile
  5

```

(2) INFORMATION FOR SEQ ID NO: 294:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..279)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..279  
id M85423  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(196..289)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 466..559  
id AA126476  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(133..194)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 560..621  
id AA126476  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(105..137)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 616..648  
id AA126476  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 152..292  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..141  
id R33928  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 160..292  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 14..146  
id H67425  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 161..292  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..132  
id W04820  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 101..232  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq IALTLIPSMLSRA/AG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

|  |             |
|--|-------------|
| AACTTCTTCA TCTTGGTGGT CCTTGCCAG TTATTTTGCC TCATTAGACA TCAAGAAATG | 60          |
| GAGAAAGACT GAAAGTTAAT ATCTTAAGTG CTTGTTCTTC ATG TTT CCT TCT TGT  | 115         |
| Met Phe Pro Ser Cys  | -40         |
| TAT TTA TGC TAT TCT CTT TGT GGC TCC ATT CTT CTT TCA ATC TTC TCA  | 163         |
| Tyr Leu Cys Tyr Ser Leu Cys Gly Ser Ile Leu Leu Ser Ile Phe Ser  | -35 -30 -25 |
| GCT TAT AAC CGT CTT TCC CTT ATG CTA AGG ATA GCC CTT ACA CTC ATC  | 211         |



Ala Tyr Asn Arg Leu Ser Leu Met Leu Arg Ile Ala Leu Thr Leu Ile  
-20 -15 -10

CCA TCT ATG CTG TCA AGG GCT GCT GGT TGG TGC TGG TAC AAG GAG CCC 259  
Pro Ser Met Leu Ser Arg Ala Ala Gly Trp Cys Trp Tyr Lys Glu Pro  
-5 1 5

ACT CAG CAG TTT TCT TAC CTT TGC CTG CCC TGC GGG 295  
Thr Gln Gln Phe Ser Tyr Leu Cys Leu Pro Cys Gly  
10 15 20

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(9..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 36..345  
id R32875  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(52..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 35..301  
id N69845  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(9..52)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 302..345  
id N69845  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(39..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 46..325  
id H20723

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(30..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 35..323  
id HSC3JH072  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(65..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 43..296  
id R02144  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 125..304
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq QLXFLYFVCCIFQ/DV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

```

AAMAAGCTCC CAGCCTCCAG AGGCTCTCAA TGAAGAGTCA CCTTCATGGT CGTCTYCAGG    60
AACAGGACGG ATGAMGAAGG GGTGGGGTTA AGACTCAGGG GCACCTGAGG GTCTGAGCCC    120
CCTT ATG AGT ACC CAA GAM GGA CTG TCT ATG CAT GCA CAC CCA CAA GCC    169
  Met Ser Thr Gln Xaa Gly Leu Ser Met His Ala His Pro Gln Ala
   -60                -55                -50

TAT ACA CCA TTT ATA TAC CTA CAC GCA CGC AAG AGA CGC GGA GAG ATA    217
Tyr Thr Pro Phe Ile Tyr Leu His Ala Arg Lys Arg Arg Gly Glu Ile
  -45                -40                -35                -30

GGC GAT GCA GAC TCG CGA TTC AAT GAT CGA TAT GCT CAT AAR AGT GCT    265
Gly Asp Ala Asp Ser Arg Phe Asn Asp Arg Tyr Ala His Lys Ser Ala
           -25                -20                -15

CAA TTA TMT TTT CTG TAT TTT GTA TGC TGT ATT TTC CAA GAC GTA TAT    313
Gln Leu Xaa Phe Leu Tyr Phe Val Cys Cys Ile Phe Gln Asp Val Tyr
           -10                -5                1

TAT KTN    319
Tyr Xaa
  5

```

## (2) INFORMATION FOR SEQ ID NO: 296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: NUCLEIC ACID

- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..170)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 118..287  
id AA035134  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..170)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 116..285  
id N54275  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..170)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 119..288  
id AA088715  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(19..170)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 115..266  
id N78023  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(12..133)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 157..278  
id AA100730  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(127..170)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 119..162  
id AA100730

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 56..118
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq SSCSCSLISFTRG/DK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

```

ATCTTAGTGC CTTTATCTGT CTTTATGTCT TGGGGTTGGG GTAGGTAGAT ACCAA ATG      58
                                     Met
AAA CAC TTT CAG GAC CTT CCT TCC TCT TGC AGT TGT TCT TTA ATC TCC      106
Lys His Phe Gln Asp Leu Pro Ser Ser Cys Ser Cys Ser Leu Ile Ser
-20                               -15                -10                -5

TTT ACT AGA GGA GAT AAA TAT TTT GCA TAT AAT GAA GAA ATT TTT CTA      154
Phe Thr Arg Gly Asp Lys Tyr Phe Ala Tyr Asn Glu Glu Ile Phe Leu
          1                      5                      10

GTA TAT AAC GCA GAC CAG                                              172
Val Tyr Asn Ala Asp Gln
          15

```

## (2) INFORMATION FOR SEQ ID NO: 297:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(29..369)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 103..443  
id W26961  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(383..424)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 48..89  
id W26961  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(34..369)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 100..435  
id W26018  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(383..424)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 45..86  
id W26018  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(200..369)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 111..280  
id W26871  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(143..200)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 281..338  
id W26871  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(383..424)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 56..97  
id W26871  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(94..123)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 361..390  
id W26871  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(119..369)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 104..354  
id W26098

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(383..424)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 49..90  
id W26098  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 31..302
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..272  
id N99777  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 302..369
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 273..340  
id N99777  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 155..340
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq SILGIISVPLSIG/YC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

```

AGTGAAAAGA AGATGCCTAG AGAATGGCAA TTAAAAGAA AAAGATATAC TTGTTTGCC      60
CCTTGAÆCTG ACCGACACTG GTTCCCATGA AGCGGCTACC AAAGCTGTTT TCCAGGAGTT    120
TGGTAGAATC GACATTCTGG TCAACAATGG TGGA ATG TCC CAG CGT TCT CTG TGC      175
                               Met Ser Gln Arg Ser Leu Cys
                               -60

ATG GAT ACC AGC TTG GAT GTC TAC AGA RAG CTA ATA GAG CTT AAC TAC      223
Met Asp Thr Ser Leu Asp Val Tyr Arg Xaa Leu Ile Glu Leu Asn Tyr
-55                      -50                      -45                      -40

TTA GGG ACG GTG TCC TTG ACA AAA TGT GTT CTG CCT CAC ATG ATC GAG      271
Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His Met Ile Glu
-35                      -30                      -25

AGG AAG CAN KKA AAG ATT GTT ACT GTG AAT AGC ATC CTG GGT ATC ATA      319
Arg Lys Xaa Xaa Lys Ile Val Thr Val Asn Ser Ile Leu Gly Ile Ile
-20                      -15                      -10

TCT GTA CCT CTT TCC ATT GGA TAC TGT GCT AGC RAG CAT GCT CTS HGG      367
Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Xaa His Ala Leu Xaa

```

-5

1

5

|             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GGT         | TTT | TTT | AAT | RDH | CTT | CGA | ACA | GAD | CTT | GCC | ACA | TAC | CCA | GGT | ATA | 415 |
| Gly         | Phe | Phe | Asn | Xaa | Leu | Arg | Thr | Xaa | Leu | Ala | Thr | Tyr | Pro | Gly | Ile |     |
| 10          |     |     |     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |
| ATA GTT TCT |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 424 |
| Ile Val Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 298:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 179..348
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 160..329  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..184
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 83..164  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 383..437
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 366..420  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..66
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..46  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..383
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 324..365  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..102
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 47..83  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..215
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 81..193  
id AA076222  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 216..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 195..308  
id AA076222  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..102
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..81  
id AA076222  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 390..437
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 374..421  
id AA076222  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 324..359  
id AA076222



est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..443
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 202..404  
id AA149750  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 40..215
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..176  
id AA149750  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..443
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 181..383  
id W63593  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..184
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 3..124  
id W63593  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 179..243
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 120..184  
id W63593  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 320..438
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 267..385  
id AA130386  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 216..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 164..276  
id AA130386  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 103..215  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 50..162  
id AA130386  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 82..375  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq LALRTSWISSVCS/VT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

```

AAGTGACGCG GCCCAAGGGC GGAAGTGAGA AAGTTGTCTG CGTCTCGAGG CGAGTTGGCG      60
GACTGTGCGC GCGGCGGGGC G ATG GGG GGC TCG GGC AGT CGC CTG TCC AAG      111
                        Met Gly Gly Ser Gly Ser Arg Leu Ser Lys
                        -95                               -90

GAG CTG CTG GCC GAR TAC CAG GAC TTG ACG TTC CTG ACG AAG CAG GAG      159
Glu Leu Leu Ala Glu Tyr Gln Asp Leu Thr Phe Leu Thr Lys Gln Glu
                        -85                               -75

ATC CTC CTA GCC CAC AGG CGG TTT TGT GAG CTG CTT CCC CAG GAG CAG      207
Ile Leu Leu Ala His Arg Arg Phe Cys Glu Leu Leu Pro Gln Glu Gln
                        -70                               -60

CGG ASK NGG AGT CGT CAC TTC GGG CAC AAG TGC CCT TCG AGC AGA TTC      255
Arg Xaa Xaa Ser Arg His Phe Gly His Lys Cys Pro Ser Ser Arg Phe
                        -55                               -45

TCA GCE TTC CAG AGC TCA AGG CCA ACC CCT TCA AGG AGC GAA TCT GCA      303
Ser Ala Phe Gln Ser Ser Arg Pro Thr Pro Ser Arg Ser Glu Ser Ala
                        -35                               -25

GGG TCT TCT CCA CAT CCC CAG CCA AAG ACA GCC TTA GCT TTG AGG ACT      351
Gly Ser Ser Pro His Pro Gln Pro Lys Thr Ala Leu Ala Leu Arg Thr
                        -20                               -10

TCC TGG ATC TCC TCA GTG TGT TCA GTG ACA CAG CCA CGC CAG ACA TCA      399
Ser Trp Ile Ser Ser Val Cys Ser Val Thr Gln Pro Arg Gln Thr Ser
                        -5                               1                               5

AGT CCC ATT ATG CCT TCC GCA TCT TTG ACT TTG ATG ATG ACG      441
Ser Pro Ile Met Pro Ser Ala Ser Leu Thr Leu Met Met Thr
                        10                               15                               20

```

## (2) INFORMATION FOR SEQ ID NO: 299:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 284 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: DOUBLE  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 2..162  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 9..169  
                            id N76992  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 162..280  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 98  
                            region 168..286  
                            id N76992  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 2..113  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 8..119  
                            id W39234  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 173..280  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 100  
                            region 176..283  
                            id W39234  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 113..162  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 98  
                            region 118..167  
                            id W39234  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 20..160  
    (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..141  
id R06371  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 193..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 173..260  
id R06371  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 159..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 138..174  
id R06371  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 20..159  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..140  
id R06399  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 161..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 141..260  
id R06399  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 27..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..139  
id AA043154  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 166..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 141..255  
id AA043154  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

- (B) LOCATION: 132..215  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.6  
 seq PLSDSWALLPASA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```

AACAACTTCC GGCCCCACTG AGCGGTGTCC TGAGCCGATT ACAGCTAGGT AGTGGAGCGC    60
CGCTGCTTAC CTGGGTGCAG GAGACAGCCG GAGTCGCTGG GGGAGCTCCG CGCCGCCGGA    120
CGCCCGTGAC C ATG TGG AGG CTG CTG GCT CGC GCT AGT GCG CCG CTC CTG    170
           Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu
           -25                               -20

CGG GTG CCC TTG TCA GAT TCC TGG GCA CTC CTC CCC GCC AGT GCT GGC    218
Arg Val Pro Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly
-15                               -5                               1

GTA AAG ACA CTG CTC CCA GTA CCA AGT TTT GAA GAT GTT TCC ATT CCT    266
Val Lys Thr Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro
           5                               10                               15

GAA AAA CCC AAG CTA CTG                                           284
Glu Lys Pro Lys Leu Leu
           20
  
```

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other  
 (B) LOCATION: 169..332  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
 region 163..326  
 id H71676  
 est

(ix) FEATURE:

- (A) NAME/KEY: other  
 (B) LOCATION: 92..170  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
 region 87..165  
 id H71676  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 20..85  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 18..83  
                           id H71676  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 334..364  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 330..360  
                           id H71676  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 264..376  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 3..115  
                           id AA020192  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 6..347  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.6  
                           seq ATFVTQALIQXYA/RI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

|   |     |
|---|-----|
| AAAAA ATG GCG GAT CAT GTG CAG AGC CTG GCC CAA CTA GAG AAT CTG TGC | 50  |
| Met Ala Asp His Val Gln Ser Leu Ala Gln Leu Glu Asn Leu Cys       |     |
| -110 -105 -100  |     |
| AAA CAG CTG TAT GAA ACC ACA GAC ACA RSC AST CGG AGC TCC SAG GCA   | 98  |
| Lys Gln Leu Tyr Glu Thr Thr Asp Thr Xaa Xaa Arg Ser Ser Xaa Ala   |     |
| -95 -90 -85   |     |
| GAG AAA GCS TTG GTT GAR TTT ACC AAC AGC CCT GAT TGC CTG AGC AAG   | 146 |
| Glu Lys Ala Leu Val Glu Phe Thr Asn Ser Pro Asp Cys Leu Ser Lys   |     |
| -80 -75 -70   |     |
| TGC CAG CTA CTC CTC GAA AGA GGA AGT TCC TCT TAC TCC CAG TTA CTG   | 194 |
| Cys Gln Leu Leu Leu Glu Arg Gly Ser Ser Ser Tyr Ser Gln Leu Leu   |     |
| -65 -60 -55   |     |
| GCA GCT ACA TGC CTT ACC AAG CTT GTA TCA CGC ACA AAC AAC CCC CTA   | 242 |
| Ala Ala Thr Cys Leu Thr Lys Leu Val Ser Arg Thr Asn Asn Pro Leu   |     |
| -50 -45 -40   |     |
| CCA TTG GAA CAG CGA ATA GAT ATT CGG AAC TAT GTG CTC AAC TAS CTT   | 290 |
| Pro Leu Glu Gln Arg Ile Asp Ile Arg Asn Tyr Val Leu Asn Xaa Leu   |     |
| -35 -30 -25 -20   |     |

GCC ACT CGG CCG AAG TTG GCT ACT TTC GTG ACA CAA GCA CTT ATT CAG 338  
Ala Thr Arg Pro Lys Leu Ala Thr Phe Val Thr Gln Ala Leu Ile Gln  
-15 -10 -5

TKA TAT GCC AGA ATC ACA AAA CTG GGC TGG TTT GAC 374  
Xaa Tyr Ala Arg Ile Thr Lys Leu Gly Trp Phe Asp  
1 5

## (2) INFORMATION FOR SEQ ID NO: 301:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 2..222  
id H39781  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..173
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..158  
id AA017398  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 172..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 159..222  
id AA017398  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..220  
id AA059110  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 17..235  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 1..219  
                           id AA037143  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 56..235  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 56..235  
                           id R75754  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 14..55  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 15..56  
                           id R75754  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 62..226  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.6  
                           seq TCSVCCYLFWLIA/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

```

AACACTTCCT GGTGGATCCG AGTGAGGCGA CGGGGTAGGG GTTGGCGCTC AGGCGGCGAC      60
C ATG GCG TAT CAC GGC CTC ACT GTG CCT CTC ATT GTG ATG AGC GTG TTC      109
  Met Ala Tyr His Gly Leu Thr Val Pro Leu Ile Val Met Ser Val Phe
  -55 -                    -50                    -45                    -40

TGG GGC TTC GTC GGC TTC TTG GTG CCT TGG TTC ATC CCT AAG GGT CCT      157
Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly Pro
          -35                    -30                    -25

AAC CGG GGA GTT ATC ATT ACC ATG TTG GTG ACC TGT TCA GTT TGC TGC      205
Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Cys
          -20                    -15                    -10

TAT CTC TTT TGG CTG ATT GCA ATT CCG GCC TGG                        238
Tyr Leu Phe Trp Leu Ile Ala Ile Pro Ala Trp
      -5                        1

```

## (2) INFORMATION FOR SEQ ID NO: 302:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 base pairs



(B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(397..432)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 283..318  
 id H83411  
 est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 54..227  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.5  
 seq GGILMGSFQGTIA/GQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

|   |     |
|---|-----|
| ATATTTGCCC CTTACTTTAT CTTGTGCCTT GAGAAATTGC TGGGGAGAGA GGT ATG  | 56  |
| Met   |     |
| TCC ACT GGG CAG CTG TAC AGG ATG GAG GAT ATA GGG CGT TTC CAC TCC | 104 |
| Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His Ser |     |
| -55 -50 -45   |     |
| CAG CAG CCA GGT TCC CTC ACC CCA AGC TCA CCC ACT GTT GGG GAG ATT | 152 |
| Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu Ile |     |
| -40 -35 -30   |     |
| ATC TAC AAT AAC ACC AGA AAC ACA TTG GGG TGG ATT GGG GGT ATC CTT | 200 |
| Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile Leu |     |
| -25 -20 -15 -10   |     |
| ATG GGT TCT TTT CAG GGA ACC ATT GCT GGA CAA GGC ACA GGA GCC ACC | 248 |
| Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala Thr |     |
| -5 1 5  |     |
| TCC ATT TCT GAG CTC TGC AAG GGA CAA GAA CTA GAG CCA TCA GGG GCT | 296 |
| Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly Ala |     |
| 10 15 20  |     |
| GGG CTC ACT GTG GCC CCA CCC CAA GCC GTC AGC CTC CAG GGA TCA CAC | 344 |
| Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ser His |     |
| 25 30 35  |     |
| CCT GCC TTG GCT GCT ACA GCT TTT TCA CTC CAS TGC CCT AGG GGA GTT | 392 |
| Pro Ala Leu Ala Ala Thr Ala Phe Ser Leu Xaa Cys Pro Arg Gly Val |     |
| 40 45 50 55   |     |
| CAG CAS CTA ATG ATC TCT ATC TCT GAA CAT CTC TTC ATC CAT GCT     | 437 |

Gln Xaa Leu Met Ile Ser Ile Ser Glu His Leu Phe Ile His Ala  
60 65 70

## (2) INFORMATION FOR SEQ ID NO: 303:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..321  
id T31485  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 42..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..311  
id HSC38B061  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..325
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 70..260  
id T66273  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 69..140
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 5..76  
id T66273  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 6..224

id R24829  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..275
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 243..282  
id R24829  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 10..278  
id HSC2LF071  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 282..332
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq RWWCFHLQAEASA/HP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

```
ATAATAATAT CTAAAAGCT AAATTTTAAA TACCAGCTTT ACATAAATGA TTGTKGACTC   60
TGGTCTGTGT CTGACACCTT TCCAGAAAAA AGTCAATTGT TCAGGTACAC CAAAGAGGAA  120
GAAGAGCTGT GGAGGCCACC CTCTACAAAG CTTTATAGAA CTTCTGGATC TAACTCACAA  180
ACAAGCTTCC AGAAGAGACT AGAGACCTTA GGCCAGGAGA TGAAGGAGTT CAGTAGCAAA  240
GTCACACCTG TCCAATTCCC TGAGCTTTGC TCACTCAGCT A ATG GGA TGG CAA AGG   296
                                         Met Gly Trp Gln Arg
                                         -15

TGG TGG TGC TTT CAT CTT CAG GCA GAA GCC TCT GCC CAT CCC CCT CAA   344
Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser Ala His Pro Pro Gln
   -10                -5                      1

GGG CTG CAG                                     353
Gly Leu Gln
   5
```

## (2) INFORMATION FOR SEQ ID NO: 304:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 80..236

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95  
region 34..190  
id N34164  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 91..257

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 66..232  
id R89543  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 91..254

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 66..229  
id H59647  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 126..170

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5  
seq VIFFACVVRVRDG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

```
AGGTGACCTG GGCCGAGCCC TCCCGGTCGG CTAAGATTGC TGAGGAGGCG GCGGGTAGCT    60
GGCAGGCGCC GACTTCCGAA GGCCGCCGTC CGGGCGAGGT GTCCTCATGA CTTCTCTTGT    120
GGACC ATG TCC GTG ATC TTT TTT GCC TGC GTG GTA CGG GTA AGG GAT GGA    170
      Met Ser Val Ile Phe Phe Ala Cys Val Val Arg Val Arg Asp Gly
      -15                -10                -5

CTG CCC CTC TCA GCC TCT ACT GAT TTT TAC CAC ACC CAA GAT TTT TTG    218
Leu Pro Leu Ser Ala Ser Thr Asp Phe Tyr His Thr Gln Asp Phe Leu
      1                5                10                15

GAA TGG AGG AGA CGG CTC AAG AGT TTA GCC TTG CGA CTG AAG    260
Glu Trp Arg Arg Arg Leu Lys Ser Leu Ala Leu Arg Leu Lys
      20                25                30
```

## (2) INFORMATION FOR SEQ ID NO: 305:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..210
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 29..195  
id R88607  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..135
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 16..134  
id AA035300  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 134..242  
id AA035300  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..207  
id AA147873  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(128..244)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 263..379  
id AA147836  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(38..131)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 375..468  
                           id AA147836  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 136..244  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 91..199  
                           id T69348  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 45..138  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 1..94  
                           id T69348  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 66..113  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.5  
                           seq TALAAXTWLGVWG/VR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

```

AATTAGCGCG TAACGCASAG ACTGCTTGCT GCGGCAGAGA CGCCAGAKGT GCAGCTCCAG      60
CAGCA ATG GCA GTG ACG GCG TTG GCG GCG MRG ACG TGG CTT GGC GTG TGG      110
  Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp
    -15                -10                -5

GGC GTG AGG ACC ATG CAA GCC CGA GGC TTC GGC TCG GAT CAG TCC GAG      158
Gly Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu
   1                5                10                15

AAT GTC GAC CGG GGC GCG GGC TCC ATC CGG GAA GCC GGT GGG GCC TTC      206
Asn Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe
          20                25                30

GGA AAS AGA GAG CAG GCT GAA GAS SAA CGA TAT TTC                        242
Gly Xaa Arg Glu Gln Ala Glu Xaa Xaa Arg Tyr Phe
          35                40
  
```

## (2) INFORMATION FOR SEQ ID NO: 306:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 151..402

(C) IDENTIFICATION METHOD: fasta

(D) OTHER INFORMATION: identity 100.0  
region 1..252  
id HSU21128  
vrt

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 155..402

(C) IDENTIFICATION METHOD: fasta

(D) OTHER INFORMATION: identity 99.6  
region 1..248  
id HSU18728  
vrt

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 131..402

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..272  
id H27256  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 161..402

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 31..272  
id W95921  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 296..402

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 141..247  
id C17793  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 151..252

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 1..102  
id C17793  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 174..402
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..229  
id AA180902  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 199..402
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..204  
id R58323  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 235..288
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12  
seq FTLFLALIGGTSG/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

```

ACATGCCACA CCACAAGATC CCCACAATGA CATAACTCCA TTCAGAGACT GCGTGACTG      60
GGCTGGGTCT CCCCACCCCC CCCTTCAGCT CTTGTATCAC TCAGAATCTG GCAGCCAGTT    120
CCGTCCTGAC AGAGTTCACA GCATATATTG GTGGATTCTT GTCCATAGTG CATCTGCTTT    180
AAGAATTAAC GAAAGCAGTG TCAAGACAGT AAGGATTCAA ACCATTGCGC AAAA  ATG      237
                                     Met
AGT CTA AGT GCA TTT ACT CTC TTC CTG GCA TTG ATT GGT GGT ACC AGT      285
Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr Ser
      -15                      -10                      -5
GGC CAG TAC TAT GAT TAT GAT TTT CCC CTA TCA ATT TAT GGG CAA TCA      333
Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln Ser
      1                      5                      10                      15
TCA CCA AAC TGT GCA CCA GAA TGT AAC TGC CCT GAA AGC TAC CCA AGT      381
Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro Ser
      20                      25                      30
GCC ATG TAC TGT GAT GAG CTG                                          402
Ala Met Tyr Cys Asp Glu Leu
      35

```

## (2) INFORMATION FOR SEQ ID NO: 307:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID



- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 120..272
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 96.1  
region 1..151  
id HSU21128  
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..272
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 96.0  
region 1..147  
id HSU18728  
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 40..171  
id H27256  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 100..136
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..37  
id H27256  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 40..171  
id W95921  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..245
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 52..156  
id AA093526

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..136
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 2..49  
id AA093526  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..128  
id AA180902  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 20..102  
id C17793  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 206..259
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12  
seq FTLFLALIGGTSG/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

```

ATAACTCCAT TCAGAGACTG GCGTGACTGG GCTGGGTCTC CCCACCCCCC CCTTCAGCTC    60
TTGTATGACT CAGAATCTGG CAGCCAGTTC CGTCCTGACA GAGTTCACAG CATATATTGG    120
TGGATTCTTG TCCAWAAGTG GVATCTGCTT TARGAWTTAA CGAAAGCAGT GTCAAGACAG    180
TAAGGATTCA AACCATTTCG CAAAA ATG AGT CTA AGT GCA TTT ACT CTC TTC      232
                Met Ser Leu Ser Ala Phe Thr Leu Phe
                        -15                                -10

CTG GCA TTG ATT GGT GGT ACC AGT GGC CAG TAC TAT GAT TGG                274
Leu Ala Leu Ile Gly Gly Thr Ser Gly Gln Tyr Tyr Asp Trp
                -5                                1                                5

```

## (2) INFORMATION FOR SEQ ID NO: 308:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 65..433

(C) IDENTIFICATION METHOD: fasta

(D) OTHER INFORMATION: identity 100.0  
region 1..369  
id HSU21128  
vrt

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 69..433

(C) IDENTIFICATION METHOD: fasta

(D) OTHER INFORMATION: identity 99.7  
region 1..365  
id HSU18728  
vrt

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 45..433

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 1..389  
id H27256  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 75..433

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 31..389  
id W95921  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 210..433

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 141..364  
id C17793  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 65..166

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 1..102  
id C17793  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 88..433  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 1..346  
                           id AA180902  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 113..370  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 1..258  
                           id R58323  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 149..202  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 12  
                           seq FTLFLALIGGTSG/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

```

AGCTCTTGTA TCACTCAGAA TCTGGCAGCC AGTTCGCTCC TGACAGAGTT CACAGCATAT      60
ATTGGTGGAT TCTTGTCAT AGTGCATCTG CTTTAAGAAT TAACGAAAGC AGTGTCAAGA      120
CAGTAAGGAT TCAAACCATT TGCCAAAA ATG AGT CTA AGT GCA TTT ACT CTC      172
                               Met Ser Leu Ser Ala Phe Thr Leu
                               -15

TTC CTG GCA TTG ATT GGT GGT ACC AGT GGC CAG TAC TAT GAT TAT GAT      220
Phe Leu Ala Leu Ile Gly Gly Thr Ser Gly Gln Tyr Tyr Asp Tyr Asp
-10                               -5                               1                               5

TTT CCE CTA TCA ATT TAT GGG CAA TCA TCA CCA AAC TGT GCA CCA GAA      268
Phe Pro Leu Ser Ile Tyr Gly Gln Ser Ser Pro Asn Cys Ala Pro Glu
                               10                               15                               20

TGT AAC TGC CCT GAA AGC TAC CCA AGT GCC ATG TAC TGT GAT GAG CTG      316
Cys Asn Cys Pro Glu Ser Tyr Pro Ser Ala Met Tyr Cys Asp Glu Leu
                               25                               30                               35

AAA TTG AAA AGT GTA CCA ATG GTG CCT CCT GGA ATC AAG TAT CTT TAC      364
Lys Leu Lys Ser Val Pro Met Val Pro Pro Gly Ile Lys Tyr Leu Tyr
                               40                               45                               50

CTT AGG AAT AAC CAG ATT GAC CAT ATT GAT GAA AAG GCC TTT GAG AAT      412
Leu Arg Asn Asn Gln Ile Asp His Ile Asp Glu Lys Ala Phe Glu Asn
55                               60                               65                               70

GTA ACT GAT CTG CAG TGG CTC GGG      436
Val Thr Asp Leu Gln Trp Leu Gly
                               75

```

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- ```
(A) NAME/KEY: other  
(B) LOCATION: 75..345  
(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 96.3  
                        region 1..269  
                        id HUMD3A07M5  
                        vrt
```

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 51..159  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..109  
id AA121593  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 91..150  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.9  
seq LLLLLLPFLLYMA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

|                                                                 |                      |                       |                                 |     |
|-----------------------------------------------------------------|----------------------|-----------------------|---------------------------------|-----|
| AATTTGAATT                                                      | GGGGCGTGTCTAGAAAGAGA | AGCCATAGTCTGGCGAGCAAC | GCTGGAGCAT                      | 60  |
| CCCCGCTCTGG                                                     | TGCCGCTGCA           | GCCGGCAGAG            | ATG GTT GAG CTC ATG TTC CCG CTG | 114 |
|                                                                 |                      |                       | Met Val Glu Leu Met Phe Pro Leu |     |
|                                                                 |                      |                       | -20 -15                         |     |
| TTG CTC CTC CTT CTG CCC TTC CTT CTG TAT ATG GCT GCG CCC CAA ATC |                      |                       |                                 | 162 |
| Leu Leu Leu Leu Leu Pro Phe Leu Leu Tyr Met Ala Ala Pro Gln Ile |                      |                       |                                 |     |
|                                                                 | -10                  | -5                    | 1                               |     |
| AGG AAA ATG CTG TCC AGT GGG GTG TGT ACA TCA ACT GTT CAG CTT CCT |                      |                       |                                 | 210 |
| Arg Lys Met Leu Ser Ser Gly Val Cys Thr Ser Thr Val Gln Leu Pro |                      |                       |                                 |     |
| 5                                                               | 10                   | 15                    | 20                              |     |
| GGG AAA GTA GTT GTG GTC ACA GGA GCT AAT ACA GGT ATC GGG AAG GAG |                      |                       |                                 | 258 |
| Gly Lys Val Val Val Val Thr Gly Ala Asn Thr Gly Ile Gly Lys Glu |                      |                       |                                 |     |
|                                                                 | 25                   | 30                    | 35                              |     |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACA GCC AAA GAG CTG GCT CAG AGA GGA GCT CGA GTA TAT KTA GCT TNN | 306 |
| Thr Ala Lys Glu Leu Ala Gln Arg Gly Ala Arg Val Tyr Xaa Ala Xaa |     |
| 40 45 50                                                        |     |
|                                                                 |     |
| NGG GAT GTG GAA AAG GGG GAA TTG GTG GCC ARA GAG ATC CAG ACC ACG | 354 |
| Xaa Asp Val Glu Lys Gly Glu Leu Val Ala Xaa Glu Ile Gln Thr Thr |     |
| 55 60 65                                                        |     |
|                                                                 |     |
| ACA GGG AAN SAG CAG GTG TTG GTG CGG RAA CTG GAC CTG TCT GAT ACT | 402 |
| Thr Gly Xaa Xaa Gln Val Leu Val Arg Xaa Leu Asp Leu Ser Asp Thr |     |
| 70 75 80                                                        |     |
|                                                                 |     |
| AAG TCT ATT CGA GCT TTT GCT                                     | 423 |
| Lys Ser Ile Arg Ala Phe Ala                                     |     |
| 85 90                                                           |     |

## (2) INFORMATION FOR SEQ ID NO: 310:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..303
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 96  
region 1..171  
id HSC1R  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..303
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98  
region 24..183  
id HUMC1R  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 181..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 1..123  
id T74375  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 170..213
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 1..44  
id T64778  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 184..228
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1  
seq LLYLLVPALEFCRA/GG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

```
AAAACTCAG ATCTTTTGTT TATGCAAATA GTTCATTCCC TCCAACATTC CTCCGGGAAT    60
GGTCCCCCCT CCACTCCACA GAAAACCCTC CCCTCCCTGC TGTGCATGAC GCGGGCTCCC    120
TCTGSACACA GKGVMCRAAG ACGCTGTCGG GAKAGCCCCA GGATTCAACA CGGGCCTTGA    180
GAA ATG TGG CTC TTG TAC CTC CTG GTG CCG GCC CTG TTC TGC AGG GCA    228
Met Trp Leu Leu Tyr Leu Leu Val Pro Ala Leu Phe Cys Arg Ala
-15                      -10                      -5

GGA GGC TCC ATT CCC ATC CCT CAG AAG TTA TTT GGG GAG GTG ACT TCC    276
Gly Gly Ser Ile Pro Ile Pro Gln Lys Leu Phe Gly Glu Val Thr Ser
1                      5                      10                      15

CCT CTG TTC CCC AAG CCT TAC CCC AAC GGG    306
Pro Leu Phe Pro Lys Pro Tyr Pro Asn Gly
20                      25
```

## (2) INFORMATION FOR SEQ ID NO: 311:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..263
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 99  
region 1..214  
id HSSPG28  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..263
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 99  
region 1..189  
id HSCRISP3G  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 51..146
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7  
seq LLFLVAGLLPSFP/AN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

```

AATATATACG GCTCTAACCT TCTCTCTCTG CACCTTCCTT CTGTCAATAG ATG AAA      56
   Met Lys

CAA ATA CTT CAT CCT GCT CTG GAA ACC ACT GCA ATG ACA TTA TTC CCA      104
Gln Ile Leu His Pro Ala Leu Glu Thr Thr Ala Met Thr Leu Phe Pro
-30                      -25                      -20                      -15

GTG CTG TTG TTC CTG GTT GCT GGG CTG CTT CCA TCT TTT CCA GCA AAT      152
Val Leu Leu Phe Leu Val Ala Gly Leu Leu Pro Ser Phe Pro Ala Asn
                      -10                      -5                      1

GAA GAT AAG GAT CCC GCT TTT ACT GCT TTG TTA ACC ACC CAA ACA CAA      200
Glu Asp Lys Asp Pro Ala Phe Thr Ala Leu Leu Thr Thr Gln Thr Gln
                    5                      10                      15

GTG CAA AGG GAG ATT GTG AAT AAG CAC AAT GAA CTG AGG AGA GCA GTA      248
Val Gln Arg Glu Ile Val Asn Lys His Asn Glu Leu Arg Arg Ala Val
                20                      25                      30

TCT CCC CCT GCC AAA      263
Ser Pro Pro Ala Lys
35

```

## (2) INFORMATION FOR SEQ ID NO: 312:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..467



(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 97  
region 1..335  
id HSU03877  
vrt

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 213..467  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 232..486  
id AA150097  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 35..204  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 55..224  
id AA150097  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 43..467  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 56..480  
id AA155808  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 43..404  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 73..434  
id AA147966  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 395..467  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 424..496  
id AA147966  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 51..467  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..417  
id AA058479  
est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 70..405  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 1..336  
                           id W46890  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 394..425  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 326..357  
                           id W46890  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 52..102  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.9  
                           seq LFLTMLTLALVKS/QD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

```

AACTCCCCTC GCTGCCCGGG CCCGGAGCGC ASSNGGCCGC ACAGATTCAC A ATG TTG      57
                                     Met Leu

AAA GCC CTT TTC CTA ACT ATG CTG ACT CTG GCG CTG GTC AAG TCA CAG      105
Lys Ala Leu Phe Leu Thr Met Leu Thr Leu Ala Leu Val Lys Ser Gln
-15                               -10                               -5                               1

GAC ACC GAA GAA ACC ATC ACG TAC ACG CAA TGC ACT GAC GGA TAT GAG      153
Asp Thr Glu Glu Thr Ile Thr Tyr Thr Gln Cys Thr Asp Gly Tyr Glu
          5                               10                               15

TGG GAT CCT GTG AGA CAG CAA TGC AAA GAT ATT GAT GAA TGT GAC ATT      201
Trp Asp Pro Val Arg Gln Gln Cys Lys Asp Ile Asp Glu Cys Asp Ile
          20                               25                               30

GTC CCA GAC GCT TGT AAA GGT GGA ATG AAG TGT GTC AAC CAC TAT GGA      249
Val Pro Asp Ala Cys Lys Gly Gly Met Lys Cys Val Asn His Tyr Gly
          35                               40                               45

GGA TAC CTC TGC CTT CCG AAA ACA GCC CAG ATT ATT GTC AAT AAT GAA      297
Gly Tyr Leu Cys Leu Pro Lys Thr Ala Gln Ile Ile Val Asn Asn Glu
          50                               55                               60                               65

CAG CCT CAG CAG GAA ACA CAA CCA GCA GAA GGA ACC TCA GGG GCA ACC      345
Gln Pro Gln Gln Glu Thr Gln Pro Ala Glu Gly Thr Ser Gly Ala Thr
          70                               75                               80

ACC GGG GTT GTA GCT GCC DNC AGC ATG GCA ACC AGT GBA GTG TTG MNN      393
Thr Gly Val Val Ala Ala Xaa Ser Met Ala Thr Ser Xaa Val Leu Xaa
          85                               90                               95

GGG GGT GGT TTT GTG GCC AGT GCT GCT GCA GTC GCA GGC CCT GAA ATG      441
Gly Gly Gly Phe Val Ala Ser Ala Ala Ala Val Ala Gly Pro Glu Met
          100                               105                               110

```

CAG ACT GGC CGG AAT AAC TTT GTC  
Gln Thr Gly Arg Asn Asn Phe Val  
115 120

465

## (2) INFORMATION FOR SEQ ID NO: 313:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..256
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 96  
region 1..204  
id HUMTCAYV  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..256
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 93  
region 1..207  
id MACTCRAAQ  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..256
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 94  
region 1..204  
id MACTCRAAR  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 50..115
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq LLILWFHLDCVSS/IL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

AATTTTGGCT GCAAAACGTT TTTCTGCTGT GGGTACGTGA GCAGGAAAC ATG GAG AAG 58  
Met Glu Lys  
-20

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAT CCT TTG GCA GCC CCA TTA CTA ATC CTC TGG TTT CAT CTT GAC TGC | 106 |
| Asn Pro Leu Ala Ala Pro Leu Leu Ile Leu Trp Phe His Leu Asp Cys |     |
| -15 -10 -5                                                      |     |
|                                                                 |     |
| GTG AGC AGC ATA CTG AAC GTG GAA CAA AGT CCT CAG TCA CTG CAT GTT | 154 |
| Val Ser Ser Ile Leu Asn Val Glu Gln Ser Pro Gln Ser Leu His Val |     |
| 1 5 10                                                          |     |
|                                                                 |     |
| CAG GAG GGA GAC AGC ACC AAT TTC ACC TGC AGC TTC CCT TCC AGC AAT | 202 |
| Gln Glu Gly Asp Ser Thr Asn Phe Thr Cys Ser Phe Pro Ser Ser Asn |     |
| 15 20 25                                                        |     |
|                                                                 |     |
| TTT TAT GCC TTA CAC TGG TAC AGA TGG GAA ACT GCA AAA AGC CCC GAG | 250 |
| Phe Tyr Ala Leu His Trp Tyr Arg Trp Glu Thr Ala Lys Ser Pro Glu |     |
| 30 35 40 45                                                     |     |
|                                                                 |     |
| GCC GTG                                                         | 256 |
| Ala Val                                                         |     |

## (2) INFORMATION FOR SEQ ID NO: 314:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..455
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98.7  
region 1..392  
id HSU32907  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..278  
id H09504  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 410..454
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 274..318  
id H09504

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..455
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..296  
id H17686  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 42..243  
id AA247900  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 85..123
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..39  
id AA247900  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 318..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 231..268  
id AA247900  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..231
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 22..125  
id R57541  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 231..274
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 124..167  
id R57541  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 312..455
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..144

id N87278

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 345..389
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq VVTIVILLCFCKA/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

```

AGCTGGGGCC ATGTAATTTA AAACCTCTGA AAAGTGTGCT GCGGTCCGTG CACAGCATTA    60
GTATAACGTG AGGGCTGAAT GCAGCCCATT CTCTGGAGAA CTCCTCACA CACCGCAGCM    120
AARGAGAAGG MCTGAAAGAC AAACCTGGGT GCAGCCAGAG AGGTCCAGAT AGATGAGCTT    180
GTGGCATCCA TTCCCCAAGT TCAGCCTAGG GACTCCACGT ACCCCAGCTG GGTCTCATTG    240
TTCCAGAACT GCATTAGTTA AGATTACCCA GACTTNGATT TCAAAGGAAT ACTTTCATTG    300
TTCCGTCTGT AACACGAAGT AATTGGGGCC AGCTGGATGT CAGG ATG CGT GTG GTT    356
                                   Met Arg Val Val
                                   -15

ACC ATT GTA ATC TTG CTC TGC TTT TGC AAA GCG GCT GAG CTG CGC AAA    404
Thr Ile Val Ile Leu Leu Cys Phe Cys Lys Ala Ala Glu Leu Arg Lys
   -10                      -5                      1                      5

GCA AGC CCA GGC AGT GTG AGA AGC CGA GTG AAT CAT GGC CGG GCG GGT    452
Ala Ser Pro Gly Ser Val Arg Ser Arg Val Asn His Gly Arg Ala Gly
               10                      15                      20

GGA  455
Gly

```

## (2) INFORMATION FOR SEQ ID NO: 315:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..438
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 100  
region 1..394

id HSU20350  
vrt

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 87..438  
(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 99  
region 3..352  
id HSU28934  
vrt

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 132..401  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.1  
seq LLFVATLPFWTHY/LI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

```

AAACTCTGCA AATAAAATGC TCTTAGAGGG AAGGAAAGGG AAATACTCGT CTCTGGTAAA      60
GTCTGAGCAG GACAGGGTGG CTGACTGGCA GATCCAGAGG TTCCCTTGGC AGTCCACGCC      120
AGGCCTTCAC C ATG GAT CAG TTC CCT GAA TCA GTG ACA GAA AAC TTT GAG      170
      Met Asp Gln Phe Pro Glu Ser Val Thr Glu Asn Phe Glu
      -90                      -85                      -80

TAC GAT GAT TTG GCT GAG GCC TGT TAT ATT GGG GAC ATC GTG GTC TTT      218
Tyr Asp Asp Leu Ala Glu Ala Cys Tyr Ile Gly Asp Ile Val Val Phe
      -75                      -70                      -65

GGG ACT GTG TTC CTG TCC ATA TTC TAC TCC GTC ATC TTT GCC ATT GGC      266
Gly Thr Val Phe Leu Ser Ile Phe Tyr Ser Val Ile Phe Ala Ile Gly
      -60                      -55                      -50

CTG GTG GGA AAT TTG TTG GTA GTG TTT GCC CTC ACC AAC AGC AAG AAG      314
Leu Val Gly Asn Leu Leu Val Val Phe Ala Leu Thr Asn Ser Lys Lys
      -45                      -40                      -35                      -30

CCC AAG AGT GTC ACC GAC ATT TAC CTC CTG AAC CTG GCC TTG TCT GAT      362
Pro Lys Ser Val Thr Asp Ile Tyr Leu Leu Asn Leu Ala Leu Ser Asp
      -25                      -20                      -15

CTG CTG TTT GTA GCC ACT TTG CCC TTC TGG ACT CAC TAT TTG ATA AAT      410
Leu Leu Phe Val Ala Thr Leu Pro Phe Trp Thr His Tyr Leu Ile Asn
      -10                      -5                      1

GAA AAG GGC CTC CAC AAT GCC ATG TGC      437
Glu Lys Gly Leu His Asn Ala Met Cys
      5                      10

```

## (2) INFORMATION FOR SEQ ID NO: 316:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids  
(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -23..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.4  
seq VLALLLFVHYSNG/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Met Val Phe Val His Leu Tyr Leu Gly Asn Val Leu Ala Leu Leu Leu  
-20 -15 -10

Phe Val His Tyr Ser Asn Gly Asp Glu Ser Ser Asp Pro Gly Pro Gln  
-5 1 5

His Arg Ala  
10

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -29..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.3  
seq FLLCIFLICAALA/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Met Gly Met Cys Phe Ala Ala Glu Ser Asp Val Gln Met Phe Ile Ala  
-25 -20 -15

Phe Leu Leu Cys Ile Phe Leu Ile Cys Ala Ala Leu Ala Ala Gln Lys  
-10 -5 1

Ser Gly  
5



## (2) INFORMATION FOR SEQ ID NO: 318:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11  
seq VLFLFLFWGVSLA/GS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Ala Val Arg Glu Leu Cys Phe Ser Arg Gln Arg Gln Val Leu Phe  
-25 -20 -15

Leu Phe Leu Phe Trp Gly Val Ser Leu Ala Gly Ser Gly Phe Gly Arg  
-10 -5 1 5

Tyr Ser Val Thr Gly  
10

## (2) INFORMATION FOR SEQ ID NO: 319:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7  
seq LILLALATGLVGG/ET

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val  
-15 -10 -5

Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser  
           1                          5                          10

Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly  
   15                          20                          25                          30

Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu  
                           35                          40                          45

Lys Pro Arg Tyr Gly  
                           50

## (2) INFORMATION FOR SEQ ID NO: 320:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7  
seq LILLALATGLVGG/ET

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val  
           -15                          -10                          -5

Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Xaa  
           1                          5                          10

Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly  
   15                          20                          25                          30

Ala Thr Leu Ile Ala Pro Arg Trp Leu  
                           35

## (2) INFORMATION FOR SEQ ID NO: 321:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.6  
seq SLLLAVLVFFLFA/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

```

Met Arg Ser Cys Leu Trp Arg Cys Arg His Leu Ser Gln Gly Val Gln
-30          -25          -20          -15

Trp Ser Leu Leu Leu Ala Val Leu Val Phe Phe Leu Phe Ala Leu Pro
          -10          -5          1

Ser Xaa Xaa Xaa Xaa Xaa Gln Thr Lys Pro Ser Arg His Gln Arg Thr
          5          10          15

Glu Asn Ile Lys Glu Arg Ser Leu Xaa Ser Leu Ala Lys Pro Lys Ser
20          25          30

Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile Tyr Ala Glu Pro Val
35          40          45          50

Pro Glu Asn Asn Ala Leu Asn Thr Gln Thr Gln Pro Lys Ala His Thr
          55          60          65

Thr Gly Asp Arg Arg Lys Gly
          70

```

## (2) INFORMATION FOR SEQ ID NO: 322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.6  
seq XILLALATGLVGG/EI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

```

Met Arg Ile Leu Gln Xaa Ile Leu Leu Ala Leu Ala Thr Gly Leu Val

```

-15

-10

-5

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gly | Glu | Ile | Arg | Ile | Ile | Lys | Gly | Phe | Glu | Cys | Lys | Pro | His | Ser |
|     |     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |
| Gln | Pro | Trp | Gln | Ala | Ala | Leu | Phe | Glu | Lys | Thr | Arg | Leu | Leu | Leu | Trp |
| 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |
| Gly | Asp | Ala | His | Arg | Pro | Gln | Met | Ala | Pro | Asp | Ser | Ser | Pro | Leu | Pro |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Gln | Ala | Pro | Leu | His | Ser | Ser | Pro | Gly | Ala | Ala | Gln | Pro | Pro | Glu | Gly |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -38..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 10.4  
seq LWLLKLKLVSTXWA/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

Met Leu Glu Glu Cys Gly Ala Gly Val Asp Leu Gly Phe Gly Gly Val  
-35 -30 -25  
-  
Lys Phe Ala Ser Glu Thr Pro Asn Leu Leu Trp Leu Leu Leu Lys Leu  
-20 -15 -10  
Val Ser Thr Xaa Trp Ala Val Arg Val Thr Leu Ile Ile Phe Asn Asn  
-5 1 5 10  
Gln Ala Arg

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.2  
seq RCLLLALVAESSS/QT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

Met Ile Ala Cys Ser Ile Arg Glu Leu His Arg Cys Leu Leu Leu Ala  
-20 -15 -10

Leu Val Ala Glu Ser Ser Ser Gln Thr His Gly  
-5 1

## (2) INFORMATION FOR SEQ ID NO: 325:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.2  
seq SLVLCLLSATVFS/LQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

Met Gly Pro Pro Ser Leu Val Leu Cys Leu Leu Ser Ala Thr Val Phe  
-15 -10 -5

Ser Leu Gln Gly Gly Ser Ser Ala Phe Leu Ser His His Arg Pro Gly  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO: 326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9  
seq AMWWLLLWGVQLQX/XP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

```

Met Pro Gly Pro Arg Val Trp Gly Lys Tyr Leu Trp Arg Ser Pro His
-35                               -30                -25                -20

Ser Lys Gly Cys Pro Gly Ala Met Trp Trp Leu Leu Leu Trp Gly Val
          -15                               -10                -5

Leu Gln Xaa Xaa Pro Asn Pro Gly Leu Arg Pro Leu Gly Xaa Arg Ala
          1                               5                10

Thr Pro Ala Ala Asp Ile Pro Arg Val Pro Arg Ala Val Trp Gln Arg
    15                               20                25

Pro Arg Glu Gln His Gly His Gln Gly Ser Arg Gly Leu Cys Cys Glu
    30                               35                40                45

Ala Arg Leu Pro Gly Leu Arg Pro Gly Ala Val Pro Gly Leu Cys Arg
          50                               55                60

Gly Leu Cys His Asn Leu Ile Arg Arg Phe Gly Ser Lys Pro Leu Gly
          65                               70                75

```

## (2) INFORMATION FOR SEQ ID NO: 327:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq LLTLALLGGPTWX/XK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu Leu  
           -20                          -15                          -10

Gly Gly Pro Thr Trp Xaa Xaa Lys Met Tyr Gly Pro Gly Gly Gly Lys  
       -5                                  1                                  5                                  10

Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr Gly Leu Arg  
                           15                                  20                                  25

Val Ser Val Gly Xaa Leu Leu Val Lys Ser Val Gln Val Lys Leu Gly  
                   30                                  35                                  40

Asp Ser Trp Asp Val Lys Leu Gly Gly Leu Arg Trp Glu Tyr Pro Gly  
           45                                  50                                  55

Ser His Pro Ala Ala Arg Arg Ile His His Lys Ser Leu Cys Arg Phe  
       60                                  65                                  70

Gln Ala Phe Leu  
       75

## (2) INFORMATION FOR SEQ ID NO: 328:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6  
                                   seq SVSLALLSGWVGS/RQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

Met Val Ser Val Ser Leu Ala Leu Leu Ser Gly Trp Val Gly Ser Arg  
   -15                          -10                          -5                                  1

Gln Gly Gly Val Gly Leu Ser Thr Leu Val Thr Leu Gly Leu Val Ser  
           5                                  10                                  15

Trp Cys Trp Arg Met Val Arg Thr Gln Ala Leu Glu Gly Phe Leu Ser  
       20                                  25                                  30

Val Lys Tyr Tyr Ser Ala Phe Ser Ala Asp Leu  
       35                                  40

## (2) INFORMATION FOR SEQ ID NO: 329:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5  
seq IVFLLLRVSPCLG/PS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

```

Met His Ile Phe Ser Ile Cys Cys Met Xaa Ser Glu Leu His Lys Met
      -45                      -40                      -35

Lys Ser Leu Ser Leu Gln Leu Ala Ser Glu Lys Arg Ser Leu Val Ala
      -30                      -25                      -20

Leu Val Glu Glu Ile Val Phe Leu Leu Leu Arg Val Ser Pro Cys Leu
      -15                      -10                      -5

Gly Pro Ser Xaa Lys Pro Arg
  1                      5

```

## (2) INFORMATION FOR SEQ ID NO: 330:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq VSALLMAWFGVLS/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

```

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val Leu
      -15                      -10                      -5

```



Ser Cys Val Gln Thr Gly  
 1 5

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq LLLPLMLMSMVSS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Val | Leu | Ile | Ser | Ser | Leu | Leu | Leu | Leu | Pro | Leu | Met | Leu |     |
|     |     | -20 |     |     |     |     | -15 |     |     |     | -10 |     |     |     |     |
| Met | Ser | Met | Val | Ser | Ser | Ser | Leu | Xaa | Pro | Gly | Val | Ala | Arg | Gly | His |
|     | -5  |     |     |     |     | 1   |     |     |     | 5   |     |     |     | 10  |     |
| Arg | Asp | Arg | Gly | Gln | Ala | Ser | Arg | Arg | Trp | Leu | Gln | Glu | Gly | Gly | Leu |
|     |     |     | 15  |     |     |     |     |     | 20  |     |     |     |     | 25  |     |

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq LLLPLMLMSM/SS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Leu Pro Leu Met Leu  
           -20                              -15                              -10

Met Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg Gly His  
       -5                              1                              5                              10

Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu Gly Gly Gln  
                               15                              20                              25

Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro Arg Arg Lys Phe  
                               30                              35                              40

Met Thr Val Ser Gly  
                               45

## (2) INFORMATION FOR SEQ ID NO: 333:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.2  
seq LLLLQLSLPSPTS/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

Met Leu Leu Leu Leu Gln Leu Ser Leu Pro Ser Pro Thr Ser Ser Pro  
                               -10                              -5                              1

## (2) INFORMATION FOR SEQ ID NO: 334:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1  
seq LSFKLLLLLAVALG/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

```

Met Leu Lys Met Leu Ser Phe Lys Leu Leu Leu Leu Ala Val Ala Leu
  -15                -10                -5

Gly Phe Phe Glu Gly Asp Ala Lys Phe Gly Glu
  1                5                10

```

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8  
seq LLTLALLGXXXWA/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

```

Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu Leu
  -20                -15                -10

Gly Xaa Xaa Xaa Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly Gly Lys
  -5                1                5                10

Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr Gly Leu Arg
      15                20                25

Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln Val Lys Leu Gly
      30                35                40

Asp Ser Trp Asp Val
      45

```

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -16..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8  
seq VSAVLCVCAAWC/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp Cys  
-15 -10 -5  
Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly Gly Arg  
1 5 10 15  
Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu Thr Thr Ile  
20 25 30  
Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys Phe Arg Asp Asp  
35 40 45  
Asp Tyr Phe Arg Thr Gly  
50

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -17..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.8  
seq VLWLISFFFTFDG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp  
-15 -10 -5

Gly His Gly Gly Phe Leu Gly Lys Asn Asp Gly Ile Lys Thr Lys Lys  
1 5 10 15  
Glu Leu Ile Val Asn Lys Lys Lys His Leu Gly Leu Gly  
20 25

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7  
seq ILDLICLLFITA/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Met Cys Ile Ile Leu Leu Asp Leu Ile Cys Leu Leu Phe Ile Thr Ala  
-15 -10 -5  
Cys Val Gly  
1

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -59..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq FMVFGSFFPLISC/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

Met Asp Cys Ala Ser Ile Ser Val Lys Phe Thr Ser Met Ala Thr Met  
                   -55                  -50                  -45

His Asp Leu Ser Gln Phe Trp Ala Ser Arg Gly Glu Val Thr Asn Trp  
                   -40                  -35                  -30

Trp Pro Val Gly Gln Thr Ser Leu Pro Leu Phe Tyr Leu Ala Phe Met  
                   -25                  -20                  -15

Val Phe Gly Ser Phe Phe Pro Leu Ile Ser Cys Gln Pro Gly  
           -10                  -5                  1

## (2) INFORMATION FOR SEQ ID NO: 340:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq LVLFGITAGATG/AK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

Met Thr Ala Ser Pro Asp Tyr Leu Val Val Leu Phe Gly Ile Thr Ala  
   -20                  -15                  -10                  -5

Gly Ala Thr Gly Ala Lys Leu Gly Ser Asp Glu Lys Glu Leu Ile Leu  
                   1                  5                  10

Leu Phe Trp Lys Val Val Asp Leu Ala Asn Lys Lys Val Gly Gln Leu  
           15                  20                  25

His Glu Xaa Xaa Leu Asp Arg Ile Trp  
       30                  35

## (2) INFORMATION FOR SEQ ID NO: 341:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq CVLVLAAAAGAVA/VF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Met Val Cys Val Leu Val Leu Ala Ala Ala Ala Gly Ala Val Ala Val  
-15                      -10                      -5                      1

Phe Leu Ile Leu Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr  
                         5                                      10                                      15

Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His  
                         20                                      25                                      30

Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser  
                         35                                      40                                      45

Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met Ser Ala Thr  
                         50                                      55                                      60

## (2) INFORMATION FOR SEQ ID NO: 342:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.5  
seq LMIPLLLLTPITA/TS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

Met Lys Lys Thr Gly Asp Gly Gly Thr Leu Ser Thr Glu Arg Ile Gly  
                         -40                                      -35                                      -30

Gly Ala Ala Leu Leu Ser Leu Leu Leu Lys Arg Met Lys Met Thr Leu  
                         -25                                      -20                                      -15

Met Ile Pro Leu Leu Leu Leu Thr Pro Ile Thr Ala Thr Ser Thr Ser  
           -10                              -5                              1

Arg Trp Pro Glu Ile Gly Val Val Ala Ile Arg Ser Gln Leu Arg Ala  
   5                              10                              15                              20

Leu His Thr Cys Gly Gln Glu Pro Val Pro Ala Met Gly Ser Glu Gly  
                               25                              30                              35

Ala Ala

## (2) INFORMATION FOR SEQ ID NO: 343:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.5  
seq LTFLQLLLISSLP/RE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu Gln Leu  
           -20                              -15                              -10

Leu Leu Ile Ser Ser Leu Pro Arg Glu Tyr Thr Val Ile Asn Glu Ala  
           -5                              1                              5

Cys Pro Gly Ala Glu Trp Xaa Ile Met Cys Arg Glu Cys Cys Glu Tyr  
   10                              15                              20                              25

Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu Val Val Gly Tyr  
                               30                              35                              40

Thr Ile Pro Cys Cys Arg Asn Glu Xaa Asn Glu Cys Asp Ser Cys Leu  
           45                              50                              55

Ile His Pro Gly Cys Thr Ile Phe Glu Asn Cys Xaa Ser Cys Arg Asn  
           60                              65                              70

Gly Ser Trp Gly Gly Thr Leu  
   75                              80

## (2) INFORMATION FOR SEQ ID NO: 344:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq SLLFFLLLEGGXT/EQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

Met Arg Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu  
-25 -20 -15

Leu Phe Phe Leu Leu Leu Glu Gly Gly Xaa Thr Glu Gln Val Xaa His  
-10 -5 1 5

Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu  
10 15 20

Arg Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn  
25 30 35

Cys Ile Cys Ser Glu Xaa Gly Asn Val Leu Cys Ser Arg Val Arg Cys  
40 45 50

## (2) INFORMATION FOR SEQ ID NO: 345:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq VSIMLLLVTVSDC/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val Thr Val  
                               -15                              -10                              -5

Ser Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys  
                               1                              5                              10

Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg  
           15                              20                              25

Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser  
       30                              35                              40                              45

His Lys Ile Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys  
                               50                              55                              60

Leu

## (2) INFORMATION FOR SEQ ID NO: 346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq SALLFSLLEAST/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu  
       -20                              -15                              -10

Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro  
       -5                              1                              5                              10

Xaa Thr Asn Asn Phe Xaa Asp Xaa Glu Ala Ala Leu Lys Ala His  
           15                              20                              25

## (2) INFORMATION FOR SEQ ID NO: 347:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq SALLFSLLEAST/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

```

Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu
-20                      -15                      -10

Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro
-5                      1                      5                      10

Pro Thr Asn Asn Phe Thr Asp Ile Glu Ala Ala Leu Lys Ala Gln Leu
15                      20                      25

Asp Ser Ala Asp Ile Pro Lys Ala Arg Arg Lys Arg Tyr Ile Ser Gln
30                      35                      40

Asn Asp Met Ile Ala Ile Leu Asp Tyr His Asn Gln Val Arg Gly Lys
45                      50                      55

Val Phe Pro Xaa Ala
60

```

## (2) INFORMATION FOR SEQ ID NO: 348:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq LLTLVLCVAVAYE/RQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

```

Met Asp Pro Asn Gly Gly Cys Cys Thr Leu Leu Thr Leu Val Leu Cys
-20                      -15                      -10

```

Val Ala Val Ala Tyr Glu Arg Gln Glu  
-5 1

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq LFTFSTSLPSSLS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Glu Gly Glu Ile Tyr Phe Gln Val Phe Leu Ser Leu Phe Thr Phe  
-25 -20 -15 -10  
Ser Thr Ser Leu Pro Ser Ser Leu Ser Ser Ser Ser Leu Ser Ser Ser  
-5 1 5  
Asn Gly

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq FLCMLAAIDLALS/TS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val  
 -40 -35 -30

Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met  
 -25 -20 -15 -10

Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met  
 -5 1

## (2) INFORMATION FOR SEQ ID NO: 351:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq PWFLAPWCPGTQS/NR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met Arg Glu Thr Xaa Pro Leu Pro Lys Pro Leu Lys Asp Thr Ala Pro  
 -40 -35 -30

Ser Ser His Gly Val Gly Ser Asp Ser Pro Ser Ala Thr Arg Pro Trp  
 -25 -20 -15

Phe Leu Ala Pro Trp Cys Pro Gly Thr Gln Ser Asn Arg Ile Cys His  
 -10 -5 1 5

Pro Pro Leu Ser Ser Pro Pro Asp Gln Ala Thr Cys Leu Arg Gly  
 10 15 20

## (2) INFORMATION FOR SEQ ID NO: 352:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq VLVVLALRSLGRS/CS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

```

Met Asp Arg Pro Gly Ser Leu Ser Val Phe Gly Ser Leu Pro Ala Ser
-60                               -55                               -50                               -45

Leu Gly Thr Trp Leu Ser Ser Pro Ala Trp Leu Val Asp Arg Pro Val
                               -40                               -35                               -30

Arg Ser Ala His Pro Ser Ala Asn Ser Thr Gly Val Arg Met Ser Val
                               -25                               -20                               -15

Leu Val Val Leu Ala Leu Arg Ser Leu Gly Arg Ser Cys Ser Leu Ser
                               -10                               -5                               1

Gln Ala Ala Pro Ser Arg Trp Thr Arg Ser Asn Asp Ala Pro Gln Pro
5                               10                               15                               20

Pro Gly Ser Gln His Ile Phe His Thr Xaa Val Pro Gly
                               25                               30

```

## (2) INFORMATION FOR SEQ ID NO: 353:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq VILLFSYPSCCLC/FL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

```

Met His Tyr Phe Val Ala Gly Lys Val Ile Leu Leu Phe Ser Tyr Pro
-20                               -15                               -10

Ser Cys Cys Leu Cys Phe Leu Val Tyr Arg Arg Val Ser Xaa Leu Phe
-5                               1                               5                               10

Lys Cys Phe Glu
                               15

```

## (2) INFORMATION FOR SEQ ID NO: 354:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq STVVLQVLTQATS/QD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Asp Leu Asn Ser Ala Ser Thr Val Val Leu Gln Val Leu Thr Gln  
                    -15                    -10                    -5

Ala Thr Ser Gln Asp Thr Ala Val Leu Lys Pro Ala Glu Glu Gln Leu  
                    1                            5                            10

Lys Gln Trp Glu Thr Gln Pro Gly Phe Tyr Ser Val Leu Leu Asn Ile  
            15                            20                            25

Phe Thr Asn His Gly  
            30

## (2) INFORMATION FOR SEQ ID NO: 355:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq FLCMLAAIDLALS/TS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

```

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
      -70              -65              -60

Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
      -55              -50              -45

Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
      -40              -35              -30

Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
      -25              -20              -15              -10

Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met
      -5              1

```

## (2) INFORMATION FOR SEQ ID NO: 356:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq PLFFSCSISATHS/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

```

Met Tyr Arg Leu Ser Leu Ile Ala Gly Pro Gly Ser Tyr Pro Val Leu
      -55              -50              -45

Arg Trp Gly Val Trp Asp Ile Pro Ser Ser Leu Val Gln Val Thr Tyr
      -40              -35              -30              -25

His Gln Pro Asn Leu Thr Thr Asn Leu Asp Leu Pro Leu Phe Phe Ser
      -20              -15              -10

Cys Ser Ile Ser Ala Thr His Ser Cys Val Lys Pro Pro Ser Val Ile
      -5              1              5

Ile Gly Ile Ser Ser Phe Leu Ser Phe Pro Tyr Gln Thr Leu Val
      10              15              20

```

## (2) INFORMATION FOR SEQ ID NO: 357:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq LCFLLAVAMSFF/GS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu  
                  -20                  -15                  -10

Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu  
                  -5                          1                          5

Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly  
          10                          15                          20

Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met  
          25                          30                          35                          40

Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe  
                  45                          50                          55

Pro Pro Ser Met His Phe Phe Gln Ala Lys Trp  
                  60                          65

## (2) INFORMATION FOR SEQ ID NO: 358:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq XLXXLLTPPPSYG/HQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

```

Met Pro Cys Ser Leu Thr Trp Arg Leu Pro Pro Arg Thr Cys Gln Xaa
-35                -30                -25                -20

Xaa Gly Leu Xaa Lys Ser Xaa Leu Xaa Xaa Leu Leu Thr Pro Pro Pro
                -15                -10                -5

Ser Tyr Gly His Gln Pro Gln Thr Gly Ser Gly Glu Ser Xaa Gly Ala
          1              5              10

Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys
    15              20              25

```

## (2) INFORMATION FOR SEQ ID NO: 359:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8  
seq LFLFLTSIAEXCS/TP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```

Met Val Xaa Trp Leu Val Leu Phe Ala Leu Gln Ile Tyr Ser Tyr Xaa
-40                -35                -30

Ser Thr Arg Asp Gln Pro Ala Ser Arg Xaa Arg Leu Leu Phe Leu Phe
-25                -20                -15                -10

Leu Thr Ser Ile Ala Glu Xaa Cys Ser Thr Pro Tyr Ser Leu Leu Gly
          -5              1              5

Xaa Val Phe Thr Val Ser Phe Val Ala Leu Gly Val Leu Thr Leu Cys
    10              15              20

Lys Phe Tyr Leu Gln Gly Tyr Arg Ala Phe Met Asn Asp Pro Ala Met
    25              30              35

Asn Arg Gly Gly Ala
    40

```

## (2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -18..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 6.7  
                            seq LPLLXXXSLPVGA/WL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Ala Arg His Gly Leu Pro Leu Leu Xaa Xaa Xaa Ser Leu Pro Val  
      -15                      -10                      -5

Gly Ala Trp Leu  
      1

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -37..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 6.7  
                            seq ILYILWYCSVCSS/GS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

Met Val His Leu Arg Thr Gly Leu Met Leu Met Ser Ala Asp Arg Leu  
      -35                      -30                      -25

Arg Thr Leu Tyr Tyr Thr Val Thr Ile Leu Tyr Ile Leu Trp Tyr Cys  
      -20                      -15                      -10

Ser Val Cys Ser Ser Gly Ser Leu Leu Ser Thr Ser Ile Met Lys Lys  
      -5                      1                      5                      10

Arg Met

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq ILSTVTALTFARA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

```
Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Arg Ala Leu
-15                -10                -5                1

Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser Glu Lys His Arg
      5                10                15

Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser Ala Pro Gly Ser
      20                25                30

Thr Gln Gln
      35
```

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5  
seq LTFLQXLLISLX/RE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu Gln Xaa  
                   -20                                  -15                                  -10

Leu Leu Ile Ser Ser Leu Xaa Arg Glu Tyr Thr Val Ile Asn Glu Ala  
                   -5                                          1                                          5

Arg Lys  
           10

## (2) INFORMATION FOR SEQ ID NO: 364:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4  
                                           seq FLLCXSVFTDCKG/DV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Met Glu Leu Leu Arg Val Cys Ser Phe Phe Leu Leu Cys Xaa Ser Val  
                   -20                                  -15                                  -10

Phe Thr Asp Cys Lys Gly Asp Val Leu Cys Val Lys Met Glu Gln Ser  
           -5                                          1                                          5                                          10

Gln Ile Cys Ala

## (2) INFORMATION FOR SEQ ID NO: 365:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq TWFLLLPPGQCRA/VG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Ile Val Arg Pro Arg Leu Asn Leu Thr Trp Phe Leu Leu Leu Pro  
-20 -15 -10

Pro Gly Gln Cys Arg Ala Val Gly Ala Thr Trp Pro Gly  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 366:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq MVALCCCLWKISG/CE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys Leu Trp Lys  
-15 -10 -5

Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu Leu Lys Cys  
1 5 10

Leu Leu Asp Lys Ala His Val Gly  
15 20

## (2) INFORMATION FOR SEQ ID NO: 367:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq CVCAAAXXSQSLX/XX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Xaa Xaa  
-20 -15 -10

Ser Gln Ser Leu Xaa Xaa Xaa Ala Ala Val Ala Ala Ala Gly Gly Arg  
-5 1 5 10

Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu Thr Xaa Ile  
15 20 25

Ser Gln Tyr Asp Lys Glu Xaa Gly Xaa Trp Asn Lys Phe Arg Asp Asp  
30 35 40

Xaa Tyr  
45

## (2) INFORMATION FOR SEQ ID NO: 368:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq MVALCCCLWKISG/CE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

Met Ser Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys Leu  
-20 -15 -10

Trp Lys Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu Leu  
-5 1 5 10

Lys Cys Leu Leu Asp Lys Ala His Cys Val Leu Leu Thr Pro Cys Gly

15

20

25

Tyr Ile Phe Ser Leu Ile Ser Pro Gly  
30 35

## (2) INFORMATION FOR SEQ ID NO: 369:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq LWILLGSLSCRTS/NR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

Met Ala Gln His Leu Trp Ile Leu Leu Gly Ser Leu Ser Cys Arg Thr  
-15 -10 -5

Ser Asn Arg Arg  
1

## (2) INFORMATION FOR SEQ ID NO: 370:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1  
seq LYLFSGFWTFXLG/KF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:



Met Asn Lys Glu Xaa Val Ser Xaa Glu Arg Xaa Ala Gln Val Arg Leu  
                   -25                  -20                  -15

Tyr Leu Phe Ser Gly Phe Trp Thr Phe Xaa Leu Gly Lys Phe Lys Gln  
                   -10                  -5                  1

Gly Glu Xaa Ser Tyr Xaa Xaa Ile Leu Glu Arg Leu Leu Trp Gln Gln  
   5                  10                  15                  20

Gln Tyr Xaa Gly Trp Leu Val Gly Asp Lys Arg  
                   25                  30

## (2) INFORMATION FOR SEQ ID NO: 371:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq IVFIFLILLNTAA/QV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Val Leu Trp Arg Ala Lys Ile Xaa Arg Asn Val Pro Val Thr Leu  
                   -50                  -45                  -40

Ser Glu Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys  
                   -35                  -30                  -25

Asn Tyr Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile  
                   -20                  -15                  -10

Leu Leu Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp  
   -5                  1                  5                  10

Leu Ser Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn  
                   15                  20                  25

## (2) INFORMATION FOR SEQ ID NO: 372:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -18..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6  
seq FTSVLWLTSPSQP/NT
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Leu Leu Xaa Phe Phe Thr Ser Val Leu Trp Leu Thr Ser Pro Ser  
-15 -10 -5

Gln Pro Asn Thr Cys Pro Ser Ser Leu Leu Cys Thr Tyr Pro Asn Leu  
1 5 10

Asn Pro Pro Trp  
15

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.9  
seq IILGCLALFLLLQ/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala  
-20 -15 -10

Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Trp  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq TWLGLLSFQNLHC/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly  
-45 -40 -35

Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser  
-30 -25 -20

Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe  
-15 -10 -5 1

Pro Asp Leu Pro Gly  
5

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq NTLFLHLSGLSAA/DT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Met Thr Trp Val Arg His Ala Pro Gly Lys Ser Leu Glu Trp Val Ala  
-55 -50 -45

Thr Val Thr Asp Gly Gly Asp Lys Thr Phe Tyr Ala Ala Ser Val Lys

|                                                                 |    |     |   |     |   |     |
|-----------------------------------------------------------------|----|-----|---|-----|---|-----|
| -40                                                             |    | -35 |   | -30 |   | -25 |
| Gly Arg Phe Asn Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu |    |     |   |     |   |     |
|                                                                 |    | -20 |   | -15 |   | -10 |
| His Leu Ser Gly Leu Ser Ala Ala Asp Thr Gly Trp Trp Gly Ile     |    |     |   |     |   |     |
|                                                                 | -5 |     | 1 |     | 5 |     |

## (2) INFORMATION FOR SEQ ID NO: 376:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq LTSFFSLTANCQS/AG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

|                                                                 |     |  |    |  |  |   |
|-----------------------------------------------------------------|-----|--|----|--|--|---|
| Met Leu Thr Ser Phe Phe Ser Leu Thr Ala Asn Cys Gln Ser Ala Gly |     |  |    |  |  |   |
|                                                                 | -10 |  | -5 |  |  | 1 |
| Thr Ile Ser Phe Ala Ala Phe Ser Leu Met Pro Gly                 |     |  |    |  |  |   |
|                                                                 | 5   |  | 10 |  |  |   |

## (2) INFORMATION FOR SEQ ID NO: 377:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq LTPLFFMXPTGFS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

Met Leu Leu Cys Leu Leu Thr Pro Leu Phe Phe Met Xaa Pro Thr Gly  
-15 -10 -5  
Phe Ser Ser Pro Ser Pro Gly  
1 5

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq HSLFLSLLGLCPS/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

Met Asp Asp Asp Tyr Glu Ala Tyr His Ser Leu Phe Leu Ser Leu Leu  
-20 -15 -10  
Gly Leu Cys Pro Ser Lys Thr Pro Ile Asn Glu Asn Ala Pro Val Phe  
-5 1 5 10  
Asp Pro Glu Pro Val  
15

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.7  
 seq WLVWLLLGHMVVS/QM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

Met Glu Trp Gly Lys Gln Trp Leu Val Trp Leu Leu Leu Gly His Met  
                   -15                  -10                  -5  
 Val Val Ser Gln Met Ala Thr Leu Leu Ala Arg Lys His Arg Pro Trp  
                   1                          5                          10

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -39..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.7  
 seq LTQGVWLWILVIQA/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

Met Arg Arg Gly Lys Arg Leu Leu Glu Ser Gln Ser Ser Ser Pro Lys  
                   -35                  -30                  -25  
 Ala Cys Leu Gln Leu Gly Phe Glu Thr Glu Leu Thr Gln Gly Val Leu  
                   -20                  -15                  -10  
 Trp Ile Leu Val Ile Gln Ala Val Pro Val Pro Ser Leu Thr Lys Thr  
                   -5                          1                          5  
 Lys  
 10

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq ALLESVVWLPCHG/RG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met Val Ala Ala Thr Glu Ala Ala Leu Leu Glu Ser Val Val Trp Leu  
-20 -15 -10 -5

Pro Cys His Gly Arg Gly Gly Ser  
1

## (2) INFORMATION FOR SEQ ID NO: 382:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq VSLPLLSSWGSTA/WT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

Met Ser Trp Asn Pro Ser Val Ser Leu Pro Leu Leu Ser Ser Trp Gly  
-15 -10 -5

Ser Thr Ala Trp Thr Leu  
1

## (2) INFORMATION FOR SEQ ID NO: 383:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq LILLSLHLERRWT/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

```

Met Lys Arg Ile Gln Gly Ile Leu Phe Leu Ile Leu Leu Ser Leu His
  -20                      -15                      -10

Leu Glu Arg Arg Trp Thr Ser Pro Ser Asp His Ser Leu Leu Leu Gly
  -5                      1                      5                      10

Gly Asn Ser Leu Ala Gln His Ala Glu Ser Val Val Arg Gln Gly
          15                      20                      25

```

## (2) INFORMATION FOR SEQ ID NO: 384:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -35..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.5  
seq LLTFGLEVCLAAG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

```

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
-35                      -30                      -25                      -20

Gln Leu Xaa Leu Xaa Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
          -15                      -10                      -5

Ala Ala Gly Ser Pro Met Cys Arg Leu Cys Cys Trp Lys Trp
          1                      5                      10

```

## (2) INFORMATION FOR SEQ ID NO: 385:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq PFALVTSCSSVFS/GD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

```

Met Ala Ala Gly Val Pro Phe Ala Leu Val Thr Ser Cys Ser Ser Val
    -15                      -10                      -5

Phe Ser Gly Asp Gln Leu Val Gln His Ile Leu Gly Thr Glu Asp Leu
    1                      5                      10

Ile Val Glu Val Thr Ser Asn Asp Ala Val Arg Phe Tyr Pro Trp Thr
    15                      20                      25                      30

Ile Asp Asn Lys Tyr Tyr Ser Ala Asp Ile Asn Leu Cys Val Val Pro
    35                      40                      45

Asn Lys Phe Leu Val Thr Ala Glu Ile Ala Glu Ser Val Gln Ala Phe
    50                      55                      60

Val Val Tyr Phe Asp Xaa Thr Gln Xaa Ser Gly Leu Asp Ser Val Ser
    65                      70                      75

Ser Trp Leu Pro Leu Ala Lys Ala Trp Leu Pro Glu Val Met Ile Leu
    80                      85                      90

Val Cys Asp Arg Val Ser Glu Asp Gly Ile
    95                      100

```

## (2) INFORMATION FOR SEQ ID NO: 386:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -14..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.5  
seq TVFLXFCFPRCHS/DS

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 386:

```
Met Thr Val Phe Leu Xaa Phe Cys Phe Pro Arg Cys His Ser Asp Ser  
          -10                      -5              1  
  
His Xaa Xaa Gln Gln Ser Ala  
      5
```

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -48..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.4  
seq ILLEVFVWNGLOG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Xaa | Pro | Asn | Asn | Phe | Trp | Gln | Lys | Leu | Gly | Arg | Lys | Lys | Pro | Arg |
|     |     |     | -45 |     |     |     |     | -40 |     |     |     |     | -35 |     |     |
| Ile | Phe | Thr | Cys | Thr | Gln | Ser | Ser | Thr | Gly | Glu | Ala | Ala | Val | Lys | Ala |
|     |     | -30 |     |     |     | -25 |     |     |     |     |     | -20 |     |     |     |
| Glu | Asn | Leu | Ile | Leu | Leu | Glu | Val | Phe | Val | Trp | Asn | Gly | Leu | Gln | Gly |
|     | -15 |     |     |     |     | -10 |     |     |     |     | -5  |     |     |     |     |
| Leu | Pro | Ser | Glu | Leu | Ser | Asp | Thr | Ser | Gly | Ser | Ser | Lys | Lys | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Val | Gly | Trp | Trp | Arg | Thr | Leu | Lys | Met | Ala | Pro | Ala | Cys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Ser | Met | Trp | Glu | Ser | Pro | Pro | Arg |     |     |     |     |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 388:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq ALYIMCVPHSVWG/CA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met Phe Arg Ser Asp Arg Met Trp Xaa Cys His Trp Lys Trp Lys Pro  
-35 -30 -25

Ser Pro Leu Leu Phe Leu Phe Ala Leu Tyr Ile Met Cys Val Pro His  
-20 -15 -10 -5

Ser Val Trp Gly Cys Ala Asn Cys Arg Val Val Leu Ser Asn Pro Ser  
1 5 10

Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser Gln  
15 20 25

Ala Cys Met Trp Thr Leu Arg Asp Pro  
30 35

## (2) INFORMATION FOR SEQ ID NO: 389:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq LVALSSELPFLGA/GV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

```

Met Thr Gln Arg Ser Ile Ala Gly Pro Ile Cys Asn Leu Lys Phe Val
-30                -25                -20

Thr Leu Leu Val Ala Leu Ser Ser Glu Leu Pro Phe Leu Gly Ala Gly
-15                -10                -5                1

Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu Leu Ile Ala Ile Asn
5                10                15

Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser Asn Ile Lys Glu Met
20                25                30

Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala Thr Lys Arg Arg Val
35                40                45

Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro Ala Gln
50                55                60

```

## (2) INFORMATION FOR SEQ ID NO: 390:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq IIPLLLLLLRSACN/VH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

```

Met Ile Ile Pro Leu Leu Leu Leu Leu Arg Ser Ala Cys Asn Val His
-10                -5                1

Leu Pro His Gln Thr Ala Ser Pro Ala Ser Leu Ser Pro Gln Gly Leu
5                10                15

Ala Trp Gly Leu Leu His Gly Gly Cys Ser Val Thr Val Arg
20                25                30

```

## (2) INFORMATION FOR SEQ ID NO: 391:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.3  
seq VLLLSXNLSNLIQ/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

Met Xaa Ser Pro Leu Pro Val Leu Leu Leu Ser Xaa Asn Leu Asn Leu  
-15 -10 -5

Ile Ile Gln Ser Ser  
1

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -46..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2  
seq LLTFLVFTXKLSS/LN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

Met Leu Met Cys Lys Met Leu Lys Ser Gln Lys Asn Cys Gln Glu Asn  
-45 -40 -35

Xaa Xaa Ile Lys Ile Ile Leu Phe Leu Lys Pro Met Cys Ser Pro Gln  
-30 -25 -20 -15

Tyr Leu Leu Thr Phe Leu Val Phe Thr Xaa Lys Leu Ser Ser Leu Asn  
-10 -5 1

Ile Xaa Lys Phe His  
5

## (2) INFORMATION FOR SEQ ID NO: 393:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq IIVILHCAASIIS/CP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

Met Lys Lys Lys Ser Ser Pro Asn Gln Tyr Leu His Ser Ser Leu His  
-50 -45 -40

Xaa Ile Arg Leu Phe Ser Phe Leu His Phe Ser Glu Glu Gly Val Leu  
-35 -30 -25

Leu Leu Ala Ile Asp Leu Lys Ile Ile Val Ile Leu His Cys Ala Ala  
-20 -15 -10 -5

Ser Ile Ile Ser Cys Pro Ser  
1

## (2) INFORMATION FOR SEQ ID NO: 394:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq ATSVSLEAQSCFA/WP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Phe Ser Cys Phe Phe Ser Thr Ser Leu Ala Thr Ser Val Ser Leu  
                   -20                                  -15                                  -10

Glu Ala Gln Ser Cys Phe Ala Trp Pro Leu Ile Val Ser Phe Pro Gln  
                   -5                                  1                                  5

Gly Ser Leu Leu Ser Pro Phe Leu Leu Met Ser Tyr Asn Leu Ser His  
   10                                  15                                  20                                  25

Leu Ile Tyr Ser Gly Glu Leu Asn Gly Arg Leu Tyr Ala Glu Asn Ser  
                   30                                  35                                  40

Gln Ile Cys Ile Cys Ser Pro Ala Gly  
                   45                                  50

## (2) INFORMATION FOR SEQ ID NO: 395:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -50..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq RTALILAVCCGSA/SI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Met His-His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys  
   -50                                  -45                                  -40                                  -35

Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala  
                   -30                                  -25                                  -20

Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly  
                   -15                                  -10                                  -5

Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser  
       1                                  5                                  10

Ser Gln Asp Leu Ser Gly Gln Thr Ala Pro Gly  
   15                                  20                                  25

## (2) INFORMATION FOR SEQ ID NO: 396:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq IYFFACFQALTSS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Ser Pro Cys Ile Tyr Phe Phe Ala Cys Phe Gln Ala Leu Thr Ser  
-15 -10 -5

Ser Ser Pro Pro Gln  
1

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq VSGASGFLPPARS/RI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Ala Glu Glu Met Glu Ser Ser Leu Glu Ala Xaa Phe Ser Ser Ser  
-30 -25 -20

Gly Ala Val Ser Gly Ala Ser Gly Phe Leu Pro Pro Ala Arg Ser Arg  
-15 -10 -5 1

Ile Phe Lys Ile Ile Val Ile Gly Asp Xaa Asn Val Gly Lys Thr Cys  
5 10 15

Leu Thr Tyr Arg Phe Cys Ala Gly Arg Phe Pro Asp Arg Thr Glu Ala



20

25

30

Thr Ile Gly Val Asp Phe Arg Glu Arg Ala Val Glu Ile Asp Gly Glu  
35 40 45

Arg Ile Lys Ile Gln Leu Trp Asp Thr Ala  
50 55

## (2) INFORMATION FOR SEQ ID NO: 398:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq VSGASGFLPPARS/RI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ala Glu Glu Met Glu Ser Ser Leu Glu Ala Ser Phe Ser Ser Ser  
-30 -25 -20

Gly Ala Val Ser Gly Ala Ser Gly Phe Leu Pro Pro Ala Arg Ser Arg  
-15 -10 -5 1

Ile Phe Lys Ile Ile Val Ile Gly Asp Ser Asn Val Xaa Lys Thr Cys  
5 10 15

Leu Thr Tyr Arg Phe Cys Ala Gly Arg Phe Pro Asp Arg  
20 25 30

## (2) INFORMATION FOR SEQ ID NO: 399:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -27..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5  
 seq HLSLILLKPLCLP/NN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Leu Val Leu Gly Ser Pro Leu Leu Gly Pro Leu Leu Trp His Leu  
 -25 -20 -15  
 Ser Leu Ile Leu Leu Lys Pro Leu Cys Leu Pro Asn Asn Leu Pro Leu  
 -10 -5 1 5  
 Ala Leu Gly Arg Cys Leu Cys Leu His Ser  
 10 15

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -55..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5  
 seq VLFMTTAVDLVIT/EV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met His Leu Leu Asp Leu Glu Ser Met Gly Lys Ser Ser Asp Gly Lys  
 -55 -50 -45 -40  
 Ser Tyr Val Ile Thr Gly Ser Trp Asn Pro Lys Ser Pro His Phe Gln  
 -35 -30 -25  
 Val Val Asn Glu Glu Thr Pro Lys Asp Lys Val Leu Phe Met Thr Thr  
 -20 -15 -10  
 Ala Val Asp Leu Val Ile Thr Glu Val Gln Glu Pro Val Arg Phe Leu  
 -5 1 5  
 Leu Glu Thr Lys Val Arg Val Cys Ser Pro Asn Glu Arg Leu Phe Trp  
 10 15 20 25  
 Pro Ala

## (2) INFORMATION FOR SEQ ID NO: 401:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq VLFVFSSIPTFL/FQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Glu Asn Leu Lys Asp Phe Tyr Val Leu Phe Val Phe Ser Ser Ile  
-20 -15 -10

Pro Leu Thr Phe Leu Phe Gln Lys Leu Pro Phe Val Trp Ile Xaa Glu  
-5 1 5 10

Glu Thr Leu Glu Thr Trp Tyr Leu Lys Ser Trp  
15 20

## (2) INFORMATION FOR SEQ ID NO: 402:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq LSIFSLVLPVCRM/HR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Met Pro Gln Tyr Cys Leu Ser Ile Phe Ser Leu Val Leu Pro Val Cys  
-15 -10 -5

Arg Met His Arg

1

## (2) INFORMATION FOR SEQ ID NO: 403:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq LLAFGTSCSVVLY/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Met Val Ala Pro Val Leu Glu Thr Ser His Val Phe Cys Cys Pro Asn  
-40 -35 -30

Arg Val Arg Gly Val Leu Asn Trp Ser Ser Gly Pro Arg Gly Leu Leu  
-25 -20 -15

Ala Phe Gly Thr Ser Cys Ser Val Val Leu Tyr Asp Pro Leu Gly Cys  
-10 -5 1 5

Cys Tyr Gln Leu Glu Trp Ser His Arg Pro Phe Arg  
10 15

## (2) INFORMATION FOR SEQ ID NO: 404:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -38..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq LSWLITWFGHXLS/DF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

```

Met  Pro  Ile  Ile  Asp  Gln  Val  Asn  Pro  Glu  Leu  His  Asp  Phe  Met  Gln
      -35                -30                -25

Ser  Ala  Glu  Val  Gly  Thr  Ile  Phe  Ala  Leu  Ser  Trp  Leu  Ile  Thr  Trp
      -20                -15                -10

Phe  Gly  His  Xaa  Leu  Ser  Asp  Phe  Arg  His  Val  Val  Arg  Leu  Tyr  Asp
      -5                1                5                10

Phe  Phe  Leu  Ala  Cys  His  Pro  Leu  Met  Pro  Ile  Tyr  Phe  Ala  Ala  Val
      15                20                25

Ile  Val  Leu  Tyr  Arg  Glu  Gln
      30

```

## (2) INFORMATION FOR SEQ ID NO: 405:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq GLCVLVPCSXSXX/WR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

```

Met  Glu  Thr  Xaa  Cys  Pro  Cys  Cys  Cys  Cys  Pro  Cys  Xaa  Gly  Xaa  Gly
      -45                -40                -35

Ser  Leu  Xaa  Xaa  Lys  Pro  Val  Tyr  Glu  Leu  Gln  Val  Gln  Lys  Ser  Val
      -30                -25                -20

Thr  Val  Gln  Glu  Gly  Leu  Cys  Val  Leu  Val  Pro  Cys  Ser  Xaa  Ser  Xaa
      -15                -10                -5

Xaa  Trp  Arg  Ser  Trp  Tyr  Ser  Ser  Pro  Pro  Leu  Tyr  Val  Tyr  Trp  Phe
      1                5                10                15

Arg  Asp  Gly  Glu  Ile  Pro  Tyr  Tyr  Ala  Glu  Val  Val  Ala  Thr  Asn  Asn
      20                25                30

Pro  Asp  Arg  Arg  Xaa  Lys  Xaa  Xaa  Xaa  Xaa  Xaa  Pro  Ile  Pro  Pro  Pro
      35                40                45

```

Trp Gly Cys Pro Glu Glu Glu Leu  
50 55

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq IYFFACFXXLTSS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

Met Ser Pro Cys Ile Tyr Phe Phe Ala Cys Phe Xaa Xaa Leu Thr Ser  
-15 -10 -5  
Ser Ser Pro Pro His Pro Cys Pro Lys Cys Trp Pro Ser Ser Gly Ser  
1 5 10 15  
Ile Pro Leu

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq VLKCLSFSXPSLP/GF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

Met Gly Arg Gly Glu Arg Arg His Tyr Trp Gly Pro Lys Leu Val Leu  
-25 -20 -15

Lys Cys Leu Ser Phe Ser Xaa Pro Ser Leu Pro Gly Phe Leu Trp Ser  
-10 -5 1 5

Leu

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -52..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.7  
seq LLAKALHLLKSSC/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -69..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq LGPSLSSLPSALS/LM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

Met His His Arg Met Asn Glu Met Asn Leu Ser Pro Val Gly Met Glu  
                  -65                  -60                  -55

Gln Leu Thr Ser Ser Ser Val Ser Asn Ala Leu Pro Val Ser Gly Ser  
                  -50                  -45                  -40

His Leu Gly Leu Ala Ala Ser Pro Thr His Ser Ala Ile Pro Ala Pro  
                  -35                  -30                  -25

Gly Leu Pro Val Ala Ile Pro Asn Leu Gly Pro Ser Leu Ser Ser Leu  
                  -20                  -15                  -10

Pro Ser Ala Leu Ser Leu Met Leu Pro Met Gly Xaa Gly Asp Arg Gly  
                  -5                  1                  5                  10

Val Met Cys Gly Leu  
                  15

## (2) INFORMATION FOR SEQ ID NO: 410:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq IWNLFSLFSTTT/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

Met Leu His Ser Asp Asn Ile Trp Asn Leu Phe Ser Leu Phe Ser Thr  
                  -15                  -10                  -5



Ser Thr Thr Leu Pro Arg

1

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq FHSAAGWSGGGQA/CG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Gln Pro Ala Ser Pro Pro Ala Arg Trp Ser Phe His Ser Ala Ala  
                  -20                  -15                  -10

Gly Trp Ser Gly Gly Gly Gln Ala Cys Gly Gly His Ser Cys Asp Gln  
                  -5                                  1                                  5

Val Leu Ala Val Ile Glu Leu Leu Asn Pro Leu Arg  
          10                                  15                                  20

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq LLAGSISHMFSQA/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Cys Phe Ser Phe Leu Leu Ala Gly Ser Ile Ser His Met Phe Ser  
-15 -10 -5

Gln Ala Leu Pro Leu His Ser Pro Gly Leu Pro Thr Thr Asn Arg Thr  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 413:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq SILFHCSVCLFLC/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Met Tyr Gly Phe Ile Ile Gly Leu Ser Ile Leu Phe His Cys Ser Val  
-20 -15 -10

Cys Leu Phe Leu Cys Gln Tyr His Ala Trp  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 414:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq SLLGCXLAININT/FP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Ser Phe Gly Xaa Ile Leu Thr Phe Arg Val Ser Leu Leu Gly Cys  
         -20                        -15                    -10

Xaa Leu Ala Ile Asn Ile Asn Thr Phe Pro Ser Asn Asn His Leu  
         -5                               1                       5

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq LGRLCAGSSGVXG/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq LVSIFFWEVTNA/FL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met Phe Asn Thr Ile Tyr Leu Val Ile Ser Leu Val Ser Ile Phe Phe  
           -20                    -15                    -10

Phe Trp Glu Val Thr Asn Ala Phe Leu Lys Ala Arg Arg Trp  
           -5                            1                    5

## (2) INFORMATION FOR SEQ ID NO: 417:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq SLPLTTGSSWSLS/SQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Ala Leu Pro Pro Lys Gly Cys Gly Ser Leu Pro Leu Thr Thr Gly  
           -20                    -15                    -10

Ser Ser Trp Ser Leu Ser Ser Gln Ile Gly Ser Pro Ala Ile Ser Asn  
           -5                            1                    5                    10

Pro Arg

## (2) INFORMATION FOR SEQ ID NO: 418:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -16..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3  
seq FLSWASFLAPLLR/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

Met Phe Val Phe Leu Ser Trp Ala Ser Phe Leu Ala Pro Leu Leu Arg  
-15 -10 -5

Ser Pro Phe Leu His Cys Leu Met Gly Met Pro Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -28..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3  
seq LLSCSPLXPLGKS/GF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

Met Xaa Met Lys Ser Ala Asn Lys Ile Thr Leu Leu Xaa His His Leu  
-25 -20 -15

Leu Ser Cys Ser Pro Leu Xaa Pro Leu Gly Lys Ser Gly Phe Ser Ser  
-10 -5 1

Cys Gln Arg Leu Gly Lys Arg Ala Leu Val Phe Pro Ile Xaa Lys Xaa  
5 10 15 20

Ile Ile Thr

## (2) INFORMATION FOR SEQ ID NO: 420:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq SFLLLFIVIPQTP/RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

Met Cys Asn Tyr Asn Ile Tyr Val Leu Tyr Asn Ile Gly Tyr Leu Tyr  
-30 -25 -20

His Pro Lys Ser Phe Leu Leu Leu Phe Ile Val Ile Pro Gln Thr Pro  
-15 -10 -5

Arg Pro  
1

## (2) INFORMATION FOR SEQ ID NO: 421:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq PLLAAPLLRSLLP/RX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Met Ala Val Ala Met Val Lys Leu Cys Glu Arg Ala Gly Leu Pro Leu  
-25 -20 -15

Leu Ala Ala Pro Leu Leu Arg Ser Leu Leu Pro Arg Xaa Pro Gln Pro  
 -10 -5 1 5  
 Gly Pro Ala Gln Pro Arg Ser Val Gln Gly Gln Arg Cys Pro Ala Arg  
 10 15 20  
 His Pro Pro Gly Asn Leu Val Cys Glu Arg Gly Ala Xaa Val Asn Gly  
 25 30 35  
 Val Thr Ala Gly Ala Xaa Gly Xaa Leu Arg Gly Leu His Arg Gly Xaa  
 40 45 50  
 Arg Ala Leu Gly Cys Ser Ala His Arg Pro Xaa His Ser Ala Arg Val  
 55 60 65  
 Arg Pro Pro Ala  
 70

## (2) INFORMATION FOR SEQ ID NO: 422:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -122..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq DVLLGLLKDVLLA/RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

Met Leu Asn Val Val Arg Ala Leu Arg Xaa Pro Gln Trp Cys Ala Glu  
 -120 -115 -110  
 Tyr Cys Leu Ser Ile His Tyr Gln His Gly Gly Val Ile Cys Thr Gln  
 -105 -100 -95  
 Val His Lys Gln Thr Val Val Gln Leu Ala Leu Arg Val Ala Asp Glu  
 -90 -85 -80 -75  
 Met Asp Val Asn Ile Gly His Glu Val Gly Tyr Val Ile Pro Phe Glu  
 -70 -65 -60  
 Asn Cys Cys Thr Asn Glu Thr Ile Leu Arg Tyr Cys Thr Asp Asp Met  
 -55 -50 -45  
 Leu Gln Arg Glu Met Met Ser Asn Pro Phe Leu Gly Ser Tyr Gly Val  
 -40 -35 -30

Ile Ile Leu Asp Asp Ile His Glu Arg Ser Ile Ala Thr Asp Val Leu  
-25 -20 -15  
Leu Gly Leu Leu Lys Asp Val Leu Leu Ala Arg Pro Glu Leu Lys  
-10 -5 1 5

## (2) INFORMATION FOR SEQ ID NO: 423:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq AGLCIGSTSYVHG/DI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

Met His Ala Gly Leu Glu Arg Xaa Ser Xaa Gln Lys Ala Leu Ala Gly  
-25 -20 -15  
Leu Cys Ile Gly Ser Thr Ser Tyr Val His Gly Asp Ile Leu Arg Thr  
-10 -5 1 5  
Glu Arg

## (2) INFORMATION FOR SEQ ID NO: 424:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq LLGSLSLWRWSAM/EP



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

```

Met Leu Asn Gly Pro Phe Gln His Arg Asn Ser Arg Ile Met Thr His
-35          *   -30          -25          -20

Arg Ser Ala Glu Lys Thr Leu Leu Gly Ser Leu Ser Leu Trp Arg Trp
          -15          -10          -5

Ser Ala Met Glu Pro Thr Asp Arg Cys Thr Arg Val Gly
          1          5          10

```

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -44..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.1  
seq IAVGLTCQHVSHA/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

```

Met Arg Val Lys Asp Pro Thr Lys Ala Leu Pro Glu Lys Ala Lys Arg
          -40          -35          -30

Ser Lys Arg Pro Thr Val Pro His Asp Glu Asp Ser Ser Asp Asp Ile
          -25          -20          -15

Ala Val Gly Leu Thr Cys Gln His Val Ser His Ala Ile Ser Val Asn
          -10          -5          1

His Val Lys Arg Ala Ile Ala Glu Asn Leu Trp Ser Val Cys Ser Glu
          5          10          15          20

Cys Leu Lys Glu Arg Arg Phe Tyr Asp Gly Gln Leu Val Leu Thr Ser
          25          30          35

Asp Ile Trp Leu Cys Leu Lys Cys Gly Phe Gln Gly Cys Gly Lys Asn
          40          45          50

Ser Glu Ser Gln His Ser Leu Lys His Phe Lys Ser Ser Arg Thr Glu
          55          60          65

Pro His Cys Ile Ile Ile Asn Leu Ser Thr
          70          75

```

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEOUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -28..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq FSLLLALSMLKGTG/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Pro Gln Lys Gly Leu Gly Leu Leu Gly Ile Leu Ser Gly Asp Phe  
-25 -20 -15

Ser Leu Leu Ala Leu Ser Met Leu Lys Gly Thr Gly Lys Val Gly Gly  
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -55..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq AALCGISLSQLFP/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln Pro Leu  
-55 -50 -45 -40

Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg  
-35 -30 -25

[illegible]

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq LLLSPWVTVPVWS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Leu Cys Phe Gly Asp Leu Leu Leu Ser Pro Trp Val Thr Val Pro  
-15 -10 -5

Val Trp Ser Ser Ser Pro Trp  
1

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig peptide

(B) LOCATION: -27..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4  
 seq LIYFLGLAADTYF/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

```

Met Gln Glu Asn Ala His Asn Leu Arg Leu Phe Lys Cys Leu Leu Ile
   -25                      -20                      -15

Tyr Phe Leu Gly Leu Ala Ala Asp Thr Tyr Phe Arg Ser Lys Arg Lys
   -10                      -5                      1                      5

Pro Val Ser Phe Val Val Thr Val Xaa Xaa Gly Xaa Tyr Ala Thr Gly
          10                      15                      20
  
```

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -59..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4  
 seq SVATALFPPLCIS/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

```

Met His Thr Cys Ser Leu Pro Cys Leu Leu Phe Ala Gln Leu Leu Glu
          -55                      -50                      -45

Phe Cys Ser Phe Pro Pro Asp Val Pro His Asn Cys Ala Pro Ile Val
          -40                      -35                      -30

Ser Val Arg Pro Pro Asn Ile Val Ala Ala Phe Glu Gly Cys Ser Val
          -25                      -20                      -15

Ala Thr Ala Leu Phe Pro Pro Leu Cys Ile Ser Thr Gly Asn Glu
          -10                      -5                      1
  
```

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids  
 (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -28..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4

seq PLLGVLFFQGVYI/VF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

```
Met Gln Gln Arg Gly Ala Ala Gly Ser Arg Gly Cys Ala Leu Phe Pro
      -25                      -20                      -15

Leu Leu Gly Val Leu Phe Phe Gln Gly Val Tyr Ile Val Phe Ser Leu
      -10                      -5                      1

Glu Ile Arg Ala Asp Ala His Val Arg Gly Tyr Val Gly Glu Lys Ile
      5                      10                      15                      20

Lys Leu Lys Cys Thr Phe Lys Ser Thr Ser Asp Val Thr Asp Lys Leu
      25                      30                      35

Thr Ile Asp Trp Thr Tyr Arg Pro Pro Ser Ser Ser His Thr Val Ser
      40                      45                      50

Ile Xaa His Tyr Gln Ser Phe Gln Tyr Pro Thr Thr Ala Gly Thr Phe
      55                      60                      65
```

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -39..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.9

seq LILNRS LPTASSS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Xaa | Xaa | Ser | Ile | Phe | Ile | Ser | Glu | Lys | Tyr | Gly | Leu | Cys | Pro | Ser |
|     |     |     |     | -35 |     |     |     |     | -30 |     |     |     |     | -25 |     |
| Lys | Thr | Pro | Ile | Met | Lys | Met | Leu | Pro | Ser | Leu | Ile | Leu | Asn | Arg | Ser |
|     |     |     | -20 |     |     |     |     | -15 |     |     |     |     | -10 |     |     |
| Leu | Pro | Thr | Ala | Ser | Ser | Ser | Ser | Ser | Arg | Lys | Asp | Phe | Arg | Leu | Pro |
|     |     | -5  |     |     |     |     | 1   |     |     |     | 5   |     |     |     |     |
| Gln | Thr | Arg | Arg | Arg | Ile | Ile | Met | Val | Pro | Arg | Lys | Glu | Asp | Gln | Thr |
| 10  |     |     |     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |
| Pro | Leu | Asn | Pro | Ala | Ser | Gln | Pro | Gln | Ala | Pro | Pro | Lys | Pro | Ile | Pro |
|     |     |     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |
| Ser | Xaa | Lys | Ser | Leu | Glu | Ala | Xaa | Asp | Xaa | Xaa | Xaa | Ser | Gln | Arg | Thr |
|     |     |     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |
| Xaa | Arg | Pro | Gly | Leu | Ser | Arg | Gly | Arg | Ser | Cys |     |     |     |     |     |
|     |     | 60  |     |     |     |     | 65  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -20..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.9  
seq FFWVVLFSAGCKV/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

```

Met Ala Phe Asp Val Ser Cys Phe Phe Trp Val Val Leu Phe Ser Ala
-20                               -15                -10                -5

Gly Cys Lys Val Ile Thr Ser Trp Asp Gln Met Tyr Ile Glu Lys Glu
                        1                      5                      10

Ala Asn Lys Thr Tyr Asn Cys Glu Asn Leu Gly Leu Ser Glu Ile Pro
      15                20                25

Asp Thr Leu Pro Asn Thr Thr Glu Phe Leu Glu Phe Ser Phe Asn Phe
      30                35                40

Leu Pro Thr Ile His Asn Arg Thr Ser Ser Arg
  45                50                55

```

## (2) INFORMATION FOR SEQ ID NO: 434:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -96..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq IMNLTVMMLDTAXG/KX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

```

Met Glu Val Ala Ala Asn Cys Ser Leu Arg Val Lys Arg Pro Leu Leu
-95                      -90                      -85

Asp Pro Arg Phe Glu Gly Tyr Lys Xaa Ser Leu Glu Pro Leu Pro Cys
-80                      -75                      -70                      -65

Tyr Gln Leu Glu Leu Asp Ala Ala Val Ala Xaa Val Lys Leu Arg Asp
                      -60                      -55                      -50

Asp Gln Tyr Thr Leu Glu His Met His Ala Phe Gly Met Tyr Asn Tyr
-45                      -40                      -35

Leu His Cys Asp Ser Trp Tyr Gln Asp Ser Val Tyr Tyr Ile Asp Thr
-30                      -25                      -20

Leu Gly Arg Ile Met Asn Leu Thr Val Met Leu Asp Thr Ala Xaa Gly
-15                      -10                      -5

Lys Xaa Arg Glu Val Phe Arg Leu Leu
1                      5

```

## (2) INFORMATION FOR SEQ ID NO: 435:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq VLAIGLLHIVLLS/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

```

Met Asn Val Gly Thr Ala His Xaa Xaa Val Asn Pro Asn Thr Arg Val
      -35                      -30                      -25

Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu
      -20                      -15                      -10

Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val
      -5                      1                      5

Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu
    10                      15                      20                      25

His Thr Val Lys Gly Xaa Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
      30                      35                      40

Arg Leu Leu Xaa His Xaa Xaa Ala Asp Gly Leu Trp Gly Pro Val
      45                      50                      55

```

## (2) INFORMATION FOR SEQ ID NO: 436:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq SWWTLLSSSPSFM/IS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

```

Met Glu Asn Phe Asn Met Tyr Lys Asn Lys Ser Trp Trp Thr Leu Leu
      -20                      -15                      -10

Ser Ser Ser Pro Ser Phe Met Ile Ser Phe Val Ser Ser Val Leu Pro
      -5                      1                      5

Val Leu Leu Thr Ile Ser Arg Phe Ile Leu Lys Gln Ile Pro Asp Gln
    10                      15                      20                      25

```



## (2) INFORMATION FOR SEQ ID NO: 437:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq VLAIGLLHIVLLS/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

```

Met Asn Val Gly Thr Xaa His Ser Glu Val Asn Pro Asn Thr Arg Val
      -35                      -30                      -25

Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu
      -20                      -15                      -10

Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val
      -5                      1                      5

Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu
  10                      15                      20                      25

Tyr Thr Val Lys Gly Thr
      30

```

## (2) INFORMATION FOR SEQ ID NO: 438:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8

seq AAASAVSVLLVAA/ER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

```

Met Ala Ala Ala Ser Ala Val Ser Val Leu Leu Val Ala Ala Glu Arg
      -10                      -5                      1

Asn Arg Trp His Arg Leu Pro Ser Leu Leu Leu Pro Pro Arg Thr Trp
      5                      10                      15

Val Trp Arg Gln Arg Thr Met Lys Tyr Thr Thr Ala Thr Gly Arg Asn
      20                      25                      30

Met
35

```

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -44..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq SGSGLSWARLSQS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Tyr | Ser | Lys | Ala | Ser | Gly | Ser | Pro | Val | Leu | Ser | Gln | Ala | Val |
|     |     |     |     | -40 |     |     |     |     | -35 |     |     |     |     | -30 |     |
| Pro | Gly | Glu | Asn | Ala | Ser | His | Arg | Arg | Gly | Ser | Ala | Asp | Leu | Gly | Ser |
|     |     |     | -25 |     |     |     |     | -20 |     |     |     |     | -15 |     |     |
| Gly | Ser | Gly | Leu | Ser | Trp | Ala | Arg | Leu | Ser | Gln | Ser | Arg | Ser | Glu | Ile |
|     |     | -10 |     |     |     |     | -5  |     |     |     |     | 1   |     |     |     |
| His | Ser | Ala | Gly | Pro | Pro | His | Leu | Gly | Gly | Arg | Thr | Asn | Gly | Pro | Glu |
| 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |     |     | 20  |
| Phe | Pro | Ala | Leu | Ser | Tyr | Ser | Ser | Gln | Leu | Leu | Ser | Leu | Ala | Gln | Leu |
|     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     | 35  |     |
| Arg | Gly | Arg | Gly | Ile | Thr | Glu | Val | Ser | Glu | Lys | Ser | Pro | Leu | Ile |     |
|     |     |     | 40  |     |     |     |     | 45  |     |     |     |     | 50  |     |     |

## (2) INFORMATION FOR SEQ ID NO: 440:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq RPVLLHLHQTAHA/DE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

Met Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp  
-35 -30 -25

Thr Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His  
-20 -15 -10

Gln Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His  
-5 1 5 10

Thr Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala  
15 20 25

Ile Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile  
30 35 40

His Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Gln  
45 50 55

## (2) INFORMATION FOR SEQ ID NO: 441:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7  
seq IPCAHLVCPTIG/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

```
Met Ile Ile Cys Tyr Asp Ile Pro Cys Ala His Met Leu Val Cys Pro
      -15                -10                -5

Thr Ile Gly Asp Ile Lys Phe Asp His Leu Met Lys Trp Tyr Pro Ser
      1                5                10

Asp Phe Ser Thr Glu Arg Leu
      15                20
```

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq STLASVPPAATFG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

```
Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala Ala
      -15                -10                -5

Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln Met
      1                5                10

Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro Gln
      15                20                25

Phe Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val Glu
      30                35                40                45

Lys Asn Lys Tyr Asp Ala
      50
```

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -65..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7  
seq QLEGLNWLRFWSA/QG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met Gly Glu Asp Pro Xaa Gln Pro Arg Lys Tyr Lys Lys Xaa Lys Xaa  
-65 -60 -55 -50

Glu Leu Gln Gly Asp Xaa Pro Pro Ser Ser Pro Thr Asn Asp Pro Thr  
-45 -40 -35

Val Lys Tyr Glu Thr Gln Pro Arg Phe Ile Thr Ala Thr Gly Gly Thr  
-30 -25 -20

Leu His Met Tyr Gln Leu Glu Gly Leu Asn Trp Leu Arg Phe Ser Trp  
-15 -10 -5

Ala Gln Gly Thr Xaa Gly  
1 5

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -42..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7  
seq LLGCLQCCWLQSG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Phe Tyr Val Ala Met Thr Lys Thr His Lys Arg Ile Arg Ser Leu  
-40 -35 -30

Cys Asn Ile His His Gly Leu Phe Gln Phe Thr Gln Gln Leu Leu Gly  
     -25                    -20                    -15  
 Cys Leu Gln Cys Cys Trp Leu Gln Ser Gly Arg Ala Pro Ala Thr Tyr  
     -10                    -5                    1                    5  
 Tyr Leu Val Glu Ser Ile Glu Lys Ser Ala His Gly Ser Val Leu Xaa  
             10                    15                    20  
 Thr Tyr Asp Gln Thr Gln Thr Arg Ile Gly Arg  
             25                    30

## (2) INFORMATION FOR SEQ ID NO: 445:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq XTCASXNPSQCLA/AF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

Met Val Ser Pro Lys Asp Leu Pro Leu Val Leu Leu Gln Asp Ile Lys  
     -60                    -55                    -50                    -45  
 Val Pro Ser Ser Met Thr Gly Ser His Ala Gly Asn Pro His Ile Glu  
             -40                    -35                    -30  
 Arg Asn Asp Leu Pro Arg His Gly Ser Pro Gln Phe Phe Thr Gly Xaa  
             -25                    -20                    -15  
 Thr Cys Ala Ser Xaa Asn Pro Ser Gln Cys Leu Ala Ala Phe  
             -10                    -5                    1

## (2) INFORMATION FOR SEQ ID NO: 446:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -15..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq FXSLFCLYFSCFL/HI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

Met Glu Phe Xaa Ser Leu Phe Cys Leu Tyr Phe Ser Cys Phe Leu His  
-15 -10 -5 1

Ile Ile Tyr Phe Xaa Ser Cys Phe Leu Tyr  
5 10

## (2) INFORMATION FOR SEQ ID NO: 447:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -45..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq ALLELIDSPECLS/KC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

Met Ala Leu His Phe Gln Ser Leu Ala Glu Leu Glu Xaa Leu Cys Thr  
-45 -40 -35 -30

His Leu Tyr Ile Gly Thr Asp Leu Thr Gln Arg Ile Glu Ala Glu Lys  
-25 -20 -15

Ala Leu Leu Glu Leu Ile Asp Ser Pro Glu Cys Leu Ser Lys Cys Gln  
-10 -5 1

Leu Leu Leu Glu Gln Gly Thr Thr Ser Tyr Ala Gln Leu Leu Ala Ala  
5 10 15

Thr Xaa  
20

## (2) INFORMATION FOR SEQ ID NO: 448:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq LTLLLITPSPSPL/LF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr  
-25 -20 -15

Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly  
-10 -5 1 5

Leu Ser Leu Arg Ser Ala Met Ser  
10

## (2) INFORMATION FOR SEQ ID NO: 449:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq AVSSLIAVGTSHG/LA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

Met Arg His Ser Leu Leu Lys Gly Ile Ser Ala Gln Ile Val Ser Ala  
-40 -35 -30



Ala Asp Lys Val Asp Ala Gly Leu Pro Thr Ala Ile Ala Val Ser Ser  
-25 -20 -15 -10

Leu Ile Ala Val Gly Thr Ser His Gly Leu Ala Gly  
-5 1

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq LSCFIFFYISSLC/CF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

Met Thr Leu Ser Cys Phe Ile Phe Phe Tyr Ile Ser Ser Leu Cys Cys  
-15 -10 -5 1

Phe Leu Ser Tyr Pro Thr Arg  
5

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq LCFLLP HHRLQEA/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg  
-15 -10 -5 1

Gln Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg  
5 10 15

Arg Arg Glu Lys Thr Asn Lys Trp Glu Lys Arg Lys Gly Ser Gly  
20 25 30

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -14..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq FSLFALNMPLGFC/VY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

Met Phe Ser Leu Phe Ala Leu Asn Met Pro Leu Gly Phe Cys Val Tyr  
-10 -5 1

Val Ile Phe Lys Ile His Asp Trp  
5 10

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -31..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION:  score 3.5
```

seq SVWGVLPSPACSA/DL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

Met Ala Ser Ser Pro Gly Val Ala Met His Ser Leu Trp Ala Thr Ile  
 -30 -25 -20

His Thr Ser Val Trp Gly Val Leu Pro Pro Pro Ala Cys Ser Ala Asp  
 -15 -10 -5 1

Leu Leu Phe Ser Asn Ala Cys Leu Leu Pro His Glu Ile His Leu  
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -45..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq LPRLLSLSQHSES/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

Met Ser Gln Glu Gly Ala Val Pro Ala Ser Ala Val Pro Leu Glu Glu  
 -45 -40 -35 -30

Leu Ser Ser Trp Pro Glu Glu Leu Cys Arg Arg Glu Leu Pro Ser Val  
 -25 -20 -15

Leu Pro Arg Leu Leu Ser Leu Ser Gln His Ser Glu Ser Trp Ile Glu  
 -10 -5 1

His Ile Gln Ile Leu Lys Ile Ile Val Glu Met Phe Leu Pro His Met  
 5 10 15

Asn His Leu Thr Leu Glu Gln Thr Phe Phe Ser Gln Val Leu Pro Lys  
 20 25 30 35

Thr Val Lys Leu Phe Asp  
 40

(2) INFORMATION FOR SEQ ID NO: 455:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq AAVVFAVLSIHA/TV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

```

Met Thr Arg Glu Cys Pro Ser Pro Ala Pro Gly Pro Gly Ala Pro Leu
-35                               -30                               -25

Ser Gly Ser Val Leu Ala Glu Ala Ala Val Val Phe Ala Val Val Leu
-20                               -15                               -10                               -5

Ser Ile His Ala Thr Val Trp
                        1

```

## (2) INFORMATION FOR SEQ ID NO: 456:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 14.8  
seq LLWWALLLGLAQA/CP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

```

Met Gln Glu Leu His Leu Leu Trp Trp Ala Leu Leu Leu Gly Leu Ala
                        -15                -10                -5

Gln Ala Cys Pro Glu Pro Cys Asp Cys Gly Glu Lys Tyr Gly Phe Gln
      1                5                10

```

Ile Ala Asp Cys Ala Tyr Arg Asp Leu Glu Ser Val Pro Pro Gly Phe  
 15 20 25 30  
 Pro Ala Asn Val Thr Thr Leu Ser Leu Ser Ala Asn Arg Leu Pro Gly  
 35 40 45  
 Leu Pro Glu Gly Ala Phe Arg Glu Val Pro Leu Leu Gln Ser Leu Trp  
 50 55 60  
 Leu Ala His Asn Glu  
 65

## (2) INFORMATION FOR SEQ ID NO: 457:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.6  
seq LLLLALCATGAQG/LY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Met Gly Arg Gln Ala Leu Leu Leu Leu Ala Leu Cys Ala Thr Gly Ala  
 -15 -10 -5  
 Gln Gly Leu Tyr Phe His Ile Gly Glu Thr Glu Lys Arg Cys Phe Ile  
 1 5 10  
 Glu Glu Ile Pro Asp Glu Thr Met Val Ile Gly Asn Tyr Arg Thr Gln  
 15 20 25 30  
 Met Trp Asp Lys Gln Lys Glu Val Phe Leu Pro Ser Thr Pro Gly Leu  
 35 40 45  
 Gly Met His Val Glu Val Lys Asp Pro Asp Gly Lys Val Val Leu Ser  
 50 55 60  
 Arg Gln Tyr Gly Ser Glu Gly Arg Phe Thr Phe Thr Ser His Xaa Xaa  
 65 70 75  
 Gly Asp His Gln Ile Cys Leu His Cys Gly  
 80 85

## (2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 12.7  
seq ILFLLSWSGPLEQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser  
-20 -15 -10

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg  
-5 1 5 10

Arg Leu Ala Ala Leu Glu Glu Arg  
15

(2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -27..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.8  
seq LLLLCPLSRGCCP/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Ser Cys Arg Glu Leu Thr His Arg Pro Cys Ser Pro His Leu Leu  
-25 -20 -15

Leu Leu Cys Pro Leu Ser Arg Gly Cys Cys Pro Leu Leu Leu Ser Xaa  
-10 -5 1 5

Pro Leu Xaa Gly Val Asn Leu Glu Ser Ile Leu Ser Leu Thr Leu Pro  
                   10                                  15                                  20

Pro Ser Pro Ser Ser Val Gly Leu Ser Pro Ser Val Thr Xaa Leu Thr  
                   25                                  30                                  35

Thr Ser Pro Val Ser Leu His Phe Ala Ser Xaa Leu Ala Gly  
                   40                                  45                                  50

## (2) INFORMATION FOR SEQ ID NO: 460:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5  
seq AALLLGLMMVVTG/DE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu  
                   -20                                  -15                                  -10

Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His  
                   -5                                  1                                  5                                  10

Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val  
                   15                                  20                                  25

Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys  
                   30                                  35                                  40

Xaa Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys  
                   45                                  50                                  55

Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp  
                   60                                  65                                  70

Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His  
                   75                                  80                                  85                                  90

Trp Leu Val Thr Asp Ile Lys Gly Ala  
                   95

## (2) INFORMATION FOR SEQ ID NO: 461:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3  
seq VHLLSLCSGKVYA/RM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser  
                  -20                  -15                  -10

Leu Cys Ser Gly Lys Val Tyr Ala Arg Met Ala Ser Leu Arg Gly Leu  
          -5                  1                  5

Gly

## (2) INFORMATION FOR SEQ ID NO: 462:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
seq LIFLCGAALLAVG/IW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
                  -25                  -20                  -15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val  
          -10                  -5                  1



Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
           5                          10                          15

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly  
       20                          25                          30                          35

Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr  
                           40                          45                          50

Glu Ser Lys Cys Ala Leu Val Thr Phe  
                           55                          60

## (2) INFORMATION FOR SEQ ID NO: 463:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6  
seq IVSLLGFVATVTL/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

Met Trp Ala Phe Ser Glu Leu Pro Met Pro Leu Leu Ile Asn Leu Ile  
           -25                          -20                          -15

Val Ser Leu Leu Gly Phe Val Ala Thr Val Thr Leu Ile Pro Ala Phe  
       -10                          -5                          1

Arg Gly His Phe Ile Ala Ala Arg Leu Cys Gly Gln Asp Leu Asn Lys  
       5                          10                          15                          20

Thr Ser Gln

## (2) INFORMATION FOR SEQ ID NO: 464:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq VLMRLVASAYSIA/QK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr  
                  -15                  -10                  -5

Ser Ile Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu  
                  1                      5                  10

Gly Asp Leu Gly Ile Val Glu Xaa Thr Cys Ala Thr Asp Leu Gln Thr  
          15                      20                  25

Lys Ala Asp Arg Leu Ala Gln Met Xaa Ile Cys Ser Ser Leu Ala Arg  
          30                      35                  40                  45

Lys Phe Pro Lys Leu Thr Ile Ile Gly Glu Glu Asp Leu Pro Ser Xaa  
                  50                      55                  60

Glu Val Asp Gln Glu  
                  65

## (2) INFORMATION FOR SEQ ID NO: 465:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -24..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.9  
seq VHLLSLCSGKAIC/KN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser  
                  -20                  -15                  -10

Leu Cys Ser Gly Lys Ala Ile Cys Lys Asn Gly Ile Ser Lys Arg Thr  
                  -5                      1                  5

Phe Glu Glu Ile Lys Glu Glu Ile Ala Ser Cys Gly Asp Val Ala Lys  
 10 15 20  
 Ala Ile Ile Asn Leu Ala Val Tyr Gly Lys Ala Gln Asn Arg Ser Tyr  
 25 30 35 40  
 Xaa Arg Leu Ala Leu Leu Val  
 45

## (2) INFORMATION FOR SEQ ID NO: 466:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq ALXVLPLLGLHEA/AS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met Ala Asp Thr Thr Pro Asn Gly Pro Gln Gly Ala Gly Ala Val Gln  
 -50 -45 -40  
 Phe Met Met Thr Asn Lys Leu Asp Thr Ala Met Trp Leu Ser Arg Leu  
 -35 -30 -25 -20  
 Phe Thr Val Tyr Cys Ser Ala Leu Xaa Val Leu Pro Leu Leu Gly Leu  
 -15 -10 -5  
 His Glu Ala Ala Ser Phe Tyr Gln Arg Ala Leu Leu Ala Asn Ala Leu  
 1 5 10  
 Thr Ser Ala Leu Arg Leu His Gln Arg Leu Pro His Phe Gln Leu Ser  
 15 20 25  
 Arg Ala Phe Leu Ala Gln Ala Leu Leu Glu Asp Ser Cys His Tyr Leu  
 30 35 40 45  
 Leu Tyr Ser Leu Ile Phe Val Asn Ser Tyr Pro Val Thr Met Ser Ile  
 50 55 60  
 Phe Pro Val Leu Leu Phe  
 65

## (2) INFORMATION FOR SEQ ID NO: 467:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq XVLVLSVVXXAMA/AF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

Met Arg Phe Arg His Phe Xaa Lys Xaa Ile Gly Xaa Val Leu Val Leu  
-20 -15 -10

Ser Val Val Xaa Xaa Ala Met Ala Ala Phe Ala Val Xaa Pro Gln Gly  
-5 1 5

Pro Ala Leu Xaa Ser Glu Pro Xaa Xaa Xaa Gly Ser Pro Thr Ser Pro  
10 15 20

Lys Pro Gly Val Asn Ala Gln Phe Leu Pro Gly Phe Leu Met Gly Xaa  
25 30 35 40

Leu Pro Ala Pro Val Thr Pro Gln Pro  
45

## (2) INFORMATION FOR SEQ ID NO: 468:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq LCVEFASVASCDA/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu  
 -40 -35 -30 -25  
 Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Val Glu Phe  
 -20 -15 -10  
 Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala  
 -5 1 5  
 Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro  
 10 15 20  
 Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Glu Thr Ile Ser Glu  
 25 30 35 40  
 Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu Thr Thr Asp Ser Thr  
 45 50 55  
 Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln Gln Glu Asn Gly Ser  
 60 65 70  
 Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly Leu Asp Leu Asn Asn  
 75 80 85  
 Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr Leu Ala Leu Tyr Ser  
 90 95 100  
 Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro Pro Tyr Tyr Ser Tyr  
 105 110 115 120  
 Leu

## (2) INFORMATION FOR SEQ ID NO: 469:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -122..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq RLVVVSVPQSRA/SL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

Met Ala Ser Pro Phe Ser Gly Ala Leu Gln Leu Thr Asp Leu Asp Asp  
 -120 -115 -110

```

Phe Ile Gly Pro Ser Gln Glu Cys Ile Lys Pro Val Lys Val Glu Lys
-105                      -100                      -95

Arg Ala Gly Ser Gly Val Ala Lys Ile Arg Ile Glu Asp Asp Gly Ser
-90                      -85                      -80                      -75

Tyr Phe Gln Ile Asn Gln Asp Gly Xaa Thr Arg Arg Leu Glu Lys Ala
                      -70                      -65                      -60

Lys Val Ser Leu Asn Tyr Cys Xaa Ala Cys Ser Gly Cys Ile Thr Ser
                      -55                      -50                      -45

Ala Glu Thr Val Leu Ile Thr Gln Gln Ser His Glu Glu Leu Lys Lys
                      -40                      -35                      -30

Val Leu Asp Ala Asn Lys Met Ala Ala Pro Ser Gln Gln Arg Leu Val
-25                      -20                      -15

Val Val Ser Val Ser Pro Gln Ser Arg Ala Ser Leu Ala Ala Arg Phe
-10                      -5                      1                      5

Gln Leu Xaa Pro Thr Asp Thr Ala Arg Lys Leu Thr Ser Phe Phe Lys
10                      15                      20

```

## (2) INFORMATION FOR SEQ ID NO: 470:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq SLVAELLLGAGSG/SH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

```

Met Gly Pro Val Pro Thr Ala Val Ala Gly Ala Gly Ser Arg Leu Val
                      -40                      -35                      -30

Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser
-25                      -20                      -15

Leu Val Ala Glu Leu Leu Leu Gly Ala Gly Ser Gly Ser His Leu Gly
-10                      -5                      1

Arg Ala Trp Ser Gly Leu Gly Ser Ser Ile Ile Glu Ala Ile Val Gly
5                      10                      15                      20

```

Val Leu Leu Thr Ile Arg Pro Ser Arg Leu Glu Pro Pro Tyr His Trp  
                             25                            30                            35  
 Thr Ser Pro Ala  
                             40

## (2) INFORMATION FOR SEQ ID NO: 471:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq QFILLGTTSVVTA/AL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly  
                             -20                            -15                            -10  
 Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys  
                             -5                            1                            5  
 Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly  
   10                            15                            20                            25  
 Glu Asp Leu Lys Ser Ile Leu Ser Glu Xaa Pro Gly Lys Cys Val Pro  
                             30                            35                            40  
 Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn  
                             45                            50                            55  
 Ser Gln Phe Val Glu Asn Cys Lys  
                             60                            65

## (2) INFORMATION FOR SEQ ID NO: 472:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq IYIICFXLPPLFS/FN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

```

Met Gln Val Cys Arg Cys Ile Tyr Ile Ile Cys Phe Xaa Leu Pro Pro
      -15                -10                -5

Leu Phe Ser Phe Asn
      1

```

## (2) INFORMATION FOR SEQ ID NO: 473:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq QRLLLRFLASVIS/RK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

```

Met Ala Gln Arg Leu Leu Leu Arg Phe Leu Ala Ser Val Ile Ser Arg
-15                -10                -5                1

Lys Pro Ser Gln Gly Gln Trp Ala Thr Pro His Phe Gln Ser Pro Ala
      5                10                15

Asp Pro Thr Met Gln Ser Trp Trp Pro Asp Cys Asn Thr Gln Pro Ser
      20                25                30

Pro Asp
      35

```

## (2) INFORMATION FOR SEQ ID NO: 474:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq FLWLITRPQPVLPL/LL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

Met Leu Phe Ile Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala  
-40 -35 -30 -25

Leu Ile Cys Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile  
-20 -15 -10

Thr Arg Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Xaa  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 475:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -46..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq SHMLQLLPSKALC/LF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Tyr Pro Lys Trp Glu Ala Pro Val Thr Phe Cys Gln Leu Lys Arg  
-45 -40 -35

Glu Lys Asp Pro Pro His Pro Ala His Ser Pro Phe Leu Gln Pro Arg  
-30 -25 -20 -15

Phe Ser His Met Leu Gln Leu Leu Pro Ser Lys Ala Leu Cys Leu Phe  
                   -10                                  -5  1

Phe

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq LAERLGLFEELWA/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

Met Ala Leu Tyr Gln Arg Trp Arg Cys Leu Arg Leu Gln Gly Leu Gln  
                   -40                                  -35  -30

Ala Cys Arg Leu His Thr Ala Val Val Ser Thr Pro Pro Arg Trp Leu  
                   -25                                  -20  -15

Ala Glu Arg Leu Gly Leu Phe Glu Glu Leu Trp Ala Ala Gln Val Lys  
                   -10                                  -5  1

Arg Leu Ala Ser Met Ala Gln Lys Glu Pro Gln Thr  
   5                                  10  15

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 13.8  
seq XGLLLFLLPGLG/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

```

Met Gly Val Pro Arg Pro Gln Pro Trp Ala Xaa Gly Leu Leu Leu Phe
    -20                      -15                      -10

Leu Leu Pro Gly Ser Leu Gly Ala Glu Ser His Leu Ser Leu Leu Tyr
    -5                      1                      5

His Leu Thr Ala Val Ser Ser Pro Ala Pro Gly Thr Pro Ala Phe Trp
    10                      15                      20                      25

Val Ser Gly Trp Leu Gly Pro Gln Gln Tyr Pro Ser Xaa
    30                      35

```

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -45..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.4  
seq LVLALXLVSAALS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

```

Met Ala Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys
-45                      -40                      -35                      -30

Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro
    -25                      -20                      -15

Leu Val Leu Ala Leu Xaa Leu Val Ser Ala Ala Leu Ser Ser Val Val
    -10                      -5                      1

Ser Arg Thr Asp Ser Pro Ser Pro Thr Val Leu Asn Ser His Ile Ser
    5                      10                      15

Thr Pro Asn Val Asn Ala Leu Thr His Glu Asn Gln Thr Lys Pro Ser
    20                      25                      30                      35

Ile Ser Gln Ile Ser Thr Thr Leu Pro Pro Xaa Xaa Ser Thr Lys Xaa
    40                      45                      50

```

Ser Gly Gly Ala Xaa Val Val Pro His Pro Ser Pro Gly  
                   55                                  60

## (2) INFORMATION FOR SEQ ID NO: 479:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13  
                                   seq LLLVLLLVTRXRS/MP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe  
                   -25                                  -20                  -15

Leu Leu Leu Val Leu Leu Leu Val Thr Arg Xaa Arg Ser Met Pro Ala  
                   -10                                  -5                                  1

Ser Ser Pro Ala Ala Ser Ser Phe Tyr Cys Ala Ser Ser Ala Xaa Ser  
                   5                                  10                                  15

Arg Cys Pro Leu Ala Gly Pro Cys Arg Cys Ser Ser Pro Gly Thr Ala  
   20                                  25                                  30                                  35

Phe Leu

## (2) INFORMATION FOR SEQ ID NO: 480:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.6  
seq LLLLVQLLRFLRA/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

```

Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu
   -25                               -20                   -15

Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu
   -10                               -5                       1

Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu
   5                               10                   15           20

Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
          25                               30                   35

Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
          40                               45                   50

Ala Arg

```

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2  
seq AFLLLVALSYTLA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

```

Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser
-20                               -15                   -10           -5

Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp
          1                               5                   10

Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
          15                               20                   25

Gly Asp Gln Leu Ile Trp Thr Arg
          30                               35

```

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -40..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 11.2  
seq AFLLLVALSYTLA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asn | Tyr | Thr | Asp | Ala | Glu | Ser | Ser | Phe | Ser | Lys | Gln | Glu | Ile |
| -40 |     |     |     |     | -35 |     |     |     |     | -30 |     |     |     |     | -25 |
| Ile | Arg | Val | Ala | Met | Glu | Lys | Ile | Pro | Val | Ser | Ala | Phe | Leu | Leu | Leu |
|     |     |     |     | -20 |     |     |     |     | -15 |     |     |     |     | -10 |     |
| Val | Ala | Leu | Ser | Tyr | Thr | Leu | Ala | Arg | Asp | Thr | Thr | Val | Lys | Pro | Gly |
|     |     |     | -5  |     |     |     |     | 1   |     |     |     | 5   |     |     |     |
| Ala | Lys | Lys | Asp | Thr | Lys | Asp | Ser | Arg | Pro | Lys | Pro | Pro | Arg |     |     |
|     | 10  |     |     |     |     | 15  |     |     |     |     | 20  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -53..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 10.6  
seq FILLIFIAEVAA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Phe | Xaa | Thr | Trp | Ala | Thr | Ser | Ser | Ser | Gln | Pro | Ala | Leu | Trp |
|     |     |     | -50 |     |     |     |     | -45 |     |     |     |     | -40 |     |     |
| Ser | Leu | Leu | Leu | Val | Ser | Trp | Ala | Ala | Met | Val | Leu | Arg | Leu | Arg | Ser |
|     |     | -35 |     |     |     |     | -30 |     |     |     |     | -25 |     |     |     |
| Lys | Cys | Ala | Leu | Val | Thr | Phe | Phe | Phe | Ile | Leu | Leu | Leu | Ile | Phe | Ile |
|     | -20 |     |     |     |     | -15 |     |     |     |     | -10 |     |     |     |     |
| Ala | Glu | Val | Ala | Ala | Ala | Val | Val | Ala | Leu | Val | Tyr | Xaa | Thr | Met | Xaa |
| -5  |     |     |     |     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |
| Glu | His | Phe | Leu | Thr | Leu | Leu | Val | Val | Pro | Ala | Ile | Lys | Lys | Asp | Tyr |
|     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |
| Gly | Ser | Gln | Glu | Asp | Phe | Thr | Gln | Val | Xaa | Asn | Thr | Thr | Met | Lys | Gly |
|     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |
| Leu | Lys | Cys | Cys | Gly | Phe | Thr | Asn | Tyr | Thr | Asp | Trp |     |     |     |     |
|     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -28..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 10.5  
seq LLLLVHLLRFLRA/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Trp | Glu | Leu | Leu | Leu | Trp | Leu | Leu | Val | Leu | Cys | Ala | Leu | Leu |
|     |     |     | -25 |     |     |     |     | -20 |     |     |     |     | -15 |     |     |
| Leu | Leu | Leu | Val | His | Leu | Leu | Arg | Phe | Leu | Arg | Ala | Asp | Gly | Asp | Leu |
|     |     | -10 |     |     |     |     | -5  |     |     |     |     | 1   |     |     |     |
| Thr | Leu | Leu | Trp | Ala | Glu | Trp | Gln | Gly | Arg | Arg | Pro | Glu | Trp | Glu | Leu |
| 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |     |     | 20  |
| Thr | Asp | Met | Val | Val | Trp | Val | Thr | Gly | Ala | Ser | Ser | Gly | Ile | Gly | Glu |
|     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     | 35  |     |
| Glu | Leu | Ala | Tyr | Gln | Leu | Ser | Lys | Leu | Gly | Xaa | Ser | Leu | Val | Leu | Ser |
|     |     |     | 40  |     |     |     |     | 45  |     |     |     |     | 50  |     |     |

Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu  
           55                                60                                65

Asn Gly Asn Leu Xaa Glu Lys Asp Ile Leu Val Leu Pro Leu Gly  
       70                                75                                80

## (2) INFORMATION FOR SEQ ID NO: 485:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.3  
seq VSCLTLWSPGCWP/QP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

Met Thr Thr Phe Leu Pro Val Pro Gln Met Met Ala Gly Phe Ser Phe  
       -50                                -45                                -40

Gly Thr Phe Gly Asn Pro Pro Met Glu Ser Pro Ser Ala Trp Gln Thr  
       -35                                -30                                -25                                -20

Ile His Gln Pro Phe Ile Val Ser Cys Leu Thr Leu Trp Ser Pro Gly  
                                 -15                                -10                                -5

Cys Trp Pro Gln Pro Ile Gln Arg Lys Glu Trp Asp Ser Gly Thr Phe  
                                 1                                5                                10

Glu Asn Leu Arg Val Leu Ser Cys Ala Met Val Glu  
       15                                20                                25

## (2) INFORMATION FOR SEQ ID NO: 486:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate



## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5  
seq LVXFSLTATILG/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

```

Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln Leu
      -25                -20                -15
Val Xaa Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser Trp
      -10                -5                1
Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu Pro
      5                10                15                20
Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys Leu
      25                30                35
Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys
      40                45                50
Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln Glu
      55                60                65
Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe Phe
      70                75                80
Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly
      85                90                95                100
Leu

```

## (2) INFORMATION FOR SEQ ID NO: 487:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3  
seq VLPVILLLLGAHP/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu  
 -20 -15 -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala  
 -5 1 5 10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Xaa Pro Ile Pro Ser  
 15 20 25

Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr  
 30 35 40

Ile Phe Leu Lys Phe Asp Gly Glu Arg  
 45 50

## (2) INFORMATION FOR SEQ ID NO: 488:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -109..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.1  
seq LVLAVLFFHQLVG/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

Met Ala Ser Pro Arg Thr Val Thr Ile Val Ala Leu Ser Val Ala Leu  
 -105 -100 -95

Gly Leu Phe Phe Val Phe Met Gly Thr Ile Lys Leu Thr Pro Arg Leu  
 -90 -85 -80

Ser Lys Asp Ala Tyr Ser Glu Met Lys Arg Ala Xaa Lys Ser Tyr Val  
 -75 -70 -65

Arg Ala Leu Pro Leu Leu Lys Lys Met Gly Ile Asn Ser Ile Leu Leu  
 -60 -55 -50

Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val Met Thr  
 -45 -40 -35 -30

Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu Leu Leu  
 -25 -20 -15

Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp Pro Leu  
 -10 -5 1

Lys

## (2) INFORMATION FOR SEQ ID NO: 489:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -38..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq LLLLCALHSHIYC/IK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

Met Pro Asn Leu Ser Phe Gly Gly Leu Asp Thr Asn Gln Met Arg Val  
-35 -30 -25

Asn Phe Leu Ser Val Asp Val Cys Lys Leu Leu Leu Leu Cys Ala Leu  
-20 -15 -10

His Ser His Ile Tyr Cys Ile Lys Gln Ser Ala Leu Arg  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 490:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq XXLLLLNVGQLLA/QT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

```

Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu
-55                -50                -45                -40

Leu Met Met Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu
                -35                -30                -25

Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Xaa Xaa Leu Leu Leu Leu
                -20                -15                -10

Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr
                -5                1                5

Arg Lys Lys Thr Leu Ser Thr
10                15

```

## (2) INFORMATION FOR SEQ ID NO: 491:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -71..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6  
seq VVXFLLLLLAXLIA/TY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

```

Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys Lys Arg Arg
-70                -65                -60

Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln Pro Leu Ile
-55                -50                -45                -40

Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu Lys Glu Trp
                -35                -30                -25

Thr Ser Lys Leu Trp His Arg Xaa Xaa Ile Val Val Xaa Phe Leu Leu
                -20                -15                -10

Leu Leu Ala Xaa Leu Ile Ala Thr Tyr Tyr
                -5                1

```

## (2) INFORMATION FOR SEQ ID NO: 492:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -15..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.6  
seq LLRGLLWXQVLCA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

Met Pro Leu Leu Arg Gly Leu Leu Trp Xaa Gln Val Leu Cys Ala Gly  
-15 -10 -5 1

Pro Leu His Thr Glu  
5

(2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -20..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.4  
seq AVVGCLLVPPAEA/NK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro  
-20 -15 -10 -5

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Xaa Cys Lys Cys Ile  
1 5 10

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val  
15 20 25

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val  
30 35 40

Pro  
45

(2) INFORMATION FOR SEQ ID NO: 494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

```
Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg
          -20                -15                -10

Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro
          -5                      1                      5

Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val Ser Ala Ala
    10                15                20

Phe Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile Ala Arg Ala
    25                30                35                40

Val Gly Glu Lys Arg
          45
```

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: -108..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.9  
 seq LLGLLSAEQLAEA/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

```

Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr Leu Leu Val
      -105                      -100                      -95

Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly Asp Leu Gly
      -90                      -85                      -80

Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu Thr Asp Ile
      -75                      -70                      -65

Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly Cys Met Gly
      -60                      -55                      -50                      -45

Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu Leu Phe Val
      -40                      -35                      -30

Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Xaa Xaa Val Gln Leu
      -25                      -20                      -15

Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser Val Leu Ile
      -10                      -5                      1

Leu Phe Asn Lys Ile Asp Asn
      5                      10
  
```

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -41..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.7  
 seq LLCLGQLHHPGLG/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

```

Met Glu Leu Pro Ala Val Asn Leu Glu Ser Asp Ser Pro Arg Ser Leu
      -40                      -35                      -30

Ala Ala Asp Asn Leu Gly Leu His Cys Ile Leu Arg Leu Leu Cys Leu
  
```

-25

-20

-15

-10

Gly Gln Leu His His Pro Gly Leu Gly Arg Val Gly Cys Gly Ser Ala  
-5 1 5

Gly Leu His Arg Arg Arg  
10

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -51..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.6  
seq PALILLFALGSLG/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

Met Ala Phe Leu Arg Lys Val Tyr Ser Ile Leu Ser Leu Gln Val Leu  
-50 -45 -40

Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser Val Arg  
-35 -30 -25 -20

Thr Phe Val His Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly  
-15 -10 -5

Ser Leu Gly Ser Gly  
1

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(14) FEATURE:



(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -29...-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.6  
 seq PTLAIALAANAWA/FV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

```

Met Tyr Thr Tyr Gly Asn Lys Gln His Asn Ser Pro Thr Trp Asp Asp
      -25                      -20                      -15

Pro Thr Leu Ala Ile Ala Leu Ala Ala Asn Ala Trp Ala Phe Val Leu
      -10                      -5                      1

Phe Tyr Val Ile Pro Glu Val Ser Gln Val Thr Lys Ser Ser Pro Glu
      5                      10                      15

Gln Ser Tyr Gln Gly Asp Met Tyr Pro Thr Arg Asp Leu
      20                      25                      30
  
```

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -32...-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.6  
 seq WILVLALPLTVWP/WL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

```

Met Gln Gln Ile Phe Ile Gln Gln Cys Arg Glu Leu Asn Phe Trp Ser
      -30                      -25                      -20

Arg Glu Pro Trp Ile Leu Val Leu Ala Leu Pro Leu Thr Val Trp Pro
      -15                      -10                      -5

Trp Leu Ser Pro Glu Ala Gln Pro Pro Leu
      1                      5                      10
  
```

(2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -15..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.5  
seq AVLLALLMAGLAL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln  
-15 -10 -5 1

Pro Gly Thr Ala Leu Leu Cys Tyr Ser Trp Xaa Ala Gln Val Xaa Asn  
5 10 15

Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys  
20 25 30

Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys  
35 40 45

Gly Cys Ser Leu Asn Cys Val Asp Xaa Ser Gln Asp Tyr Tyr Val Gly  
50 55 60 65

Lys Lys Asn Ile Thr Cys Cys Asp  
70

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -16..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.1  
seq QACLLGLFALILS/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu Ser  
 -15 -10 -5

Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr Leu Pro  
 1 5 10 15

Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu Glu Leu Ser  
 20 25 30

Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg Leu Ser Glu Leu  
 35 40 45

Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln Tyr Gly Lys Tyr Leu  
 50 55 60

Thr Arg  
 65

## (2) INFORMATION FOR SEQ ID NO: 502:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq LGSGGLGLSPGTSS/GR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Met Arg Pro Gly Gln Val Ser Leu Leu Gly Pro Asp Ala Val Ser Val  
 -25 -20 -15

Leu Gly Ser Gly Leu Gly Leu Ser Pro Gly Thr Ser Ser Gly Arg Asn  
 -10 -5 1

Pro Asp Pro Gly Ser Gly Pro Gly Thr Leu Pro Xaa Xaa Ser Xaa Gln  
 5 10 15

Asn Pro Ser Pro Ala Pro Asp Pro Pro Pro Ala Leu Leu Leu Trp Asn  
 20 25 30 35

Leu Leu Thr Gln Arg Leu Gly Thr Thr Leu Val Pro Thr Leu Cys Pro  
 40 45 50

Ala Gln Thr Leu Ile Leu Cys Pro Ala Gln Thr Leu Ile Leu Cys Pro  
 55 60 65

Xaa Leu Ile Pro Thr Leu Cys Pro Ala Leu Xaa Pro Val Leu Pro Xaa  
           70                              75                              80  
 Val Ala Leu Ser Ala Gln Pro Ser Leu Pro Ala Arg Val Gln Ser  
           85                              90                              95

## (2) INFORMATION FOR SEQ ID NO: 503:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8  
seq FTSASLLLPMSTG/MP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

Met Ile Asn Pro Ser Val Pro Ser Lys Ser Asn Ser His Pro Phe Leu  
           -30                              -25                              -20  
 Ser Thr Val Met Phe Thr Ser Ala Ser Leu Leu Leu Pro Met Ser Thr  
           -15                              -10                              -5  
 Gly Met Pro Thr Gln Asn Cys Phe Thr Pro Lys  
           1                              5                              10

## (2) INFORMATION FOR SEQ ID NO: 504:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -68..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7

seq IACLAWWIGGGSG/XN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

```

Met Ser Glu Lys Glu Xaa Asn Phe Pro Pro Leu Pro Lys Phe Ile Pro
      -65                      -60                      -55

Val Lys Pro Cys Phe Tyr Gln Asn Phe Ser Asp Glu Ile Pro Val Glu
      -50                      -45                      -40

His Gln Val Leu Val Lys Arg Ile Tyr Arg Leu Trp Met Phe Tyr Cys
      -35                      -30                      -25

Ala Thr Leu Gly Val Asn Leu Ile Ala Cys Leu Ala Trp Trp Ile Gly
      -20                      -15                      -10                      -5

Gly Gly Ser Gly Xaa Asn Phe Gly Leu Ala Phe Val Trp Leu Leu Leu
              1                      5                      10

Phe Thr Pro Cys Gly Tyr Val Cys Trp Phe Arg Pro Val Tyr Lys Ala
      15                      20                      25

Phe Arg Ala Asp Ser Ser Phe Asn Phe Met Ala Leu
      30                      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 505:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq ILRLYFFLQLAHS/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

```

Met Asn Pro Thr Lys Leu Ile Leu Lys Thr Ile Leu Arg Leu Tyr Phe
      -20                      -15                      -10

Phe Leu Gln Leu Ala His Ser Gly Tyr Thr Lys Leu Gln Lys Lys Tyr
      -5                      1                      5

Met Lys Ser Arg Tyr Glu Gln Val Asp Leu Val Gly Lys Met Xaa Gln
      10                      15                      20                      25

Lys Ala Ala Thr Thr Val Xaa His Leu Ala Ile Gln Cys His Trp

```

30

35

40

## (2) INFORMATION FOR SEQ ID NO: 506:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq SXXCFVSVPPASA/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

```

Met Ala Ser Ser Ser Pro Asp Ser Pro Cys Ser Xaa Xaa Cys Phe Val
      -20                      -15                      -10

Ser Val Pro Pro Ala Ser Ala Ile Pro Xaa Val Xaa Xaa Ala Xaa Asn
      -5                      1                      5

Ser Asp Xaa Pro Arg Asp Glu Val Gln Glu Val Val Phe Val Pro Ala
10                      15                      20                      25

Gly Thr His Thr Pro Gly Ser Arg Leu Gln Cys Thr Tyr Ile Glu Val
      30                      35                      40

Glu Gln Val Ser Lys Thr His Ala Val Ile Leu Ser Arg Pro Ser Trp
      45                      50                      55

Leu Trp Gly Ala Glu Met Gly Xaa Thr Ser Met Val Ser Ala Leu Ala
      60                      65                      70

Thr Arg Leu Cys Gly Arg Arg Ser Gln Leu Gly Arg Ala Xaa Ala Leu
      75                      80                      85

Leu Gly Met Asp Leu Leu Arg Cys Arg Pro Cys
90                      95                      100

```

## (2) INFORMATION FOR SEQ ID NO: 507:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -39..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq XLIAXLEPPGAMA/VR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

Met Xaa Pro Val Leu Ala Ala Leu Ala His Val Leu Cys Pro Tyr Met  
-35 -30 -25

Ala Pro Gly Leu Cys Arg Glu Pro Ile Arg Xaa Leu Ile Ala Xaa Leu  
-20 -15 -10

Glu Pro Pro Gly Ala Met Ala Val Arg Arg Leu Pro Ser Ala  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 508:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -45..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq PMLGLAAFRWIWS/RE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

Met Asn Asn Leu Asn Asp Pro Pro Asn Trp Asn Ile Arg Pro Asn Ser  
-45 -40 -35 -30

Arg Ala Asp Gly Gly Asp Gly Ser Arg Trp Asn Tyr Ala Leu Leu Val  
-25 -20 -15

Pro Met Leu Gly Leu Ala Ala Phe Arg Trp Ile Trp Ser Arg Glu Ser  
-10 -5 1

Gln Lys Glu Val Glu Lys Glu Arg Glu Ala Tyr Arg Arg Arg Thr Ala  
5 10 15

Ala Phe Gln Gln Asp Leu Glu Ala Lys Tyr His Ala Met Ile Ser Xaa  
 20 25 30 35  
 Asn Arg Arg Ala Val  
 40

## (2) INFORMATION FOR SEQ ID NO: 509:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6  
seq AALCSLFFFLSLQ/EI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Met Leu Leu Leu Phe Leu Ala Ala Leu Cys Ser Leu Phe Phe Phe Leu  
 -15 -10 -5  
 Ser Leu Gln Glu Ile Ala Pro Gln Asp Pro Lys Pro Gly  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO: 510:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5  
seq IIVCLFAFLVAHC/FL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:



Met Leu Phe Leu Gly Lys Val Leu Ile Val Cys Ser Thr Gly Leu Ala  
           -45                          -40                          -35

Gly Ile Met Leu Leu Asn Tyr Gln Gln Asp Tyr Thr Val Trp Val Leu  
       -30                          -25                          -20

Pro Leu Ile Ile Val Cys Leu Phe Ala Phe Leu Val Ala His Cys Phe  
       -15                          -10                          -5                          1

Leu Ser Ile Tyr Glu Met Val Val Asp Ala Arg  
                           5  10

## (2) INFORMATION FOR SEQ ID NO: 511:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -38..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
   seq LLLLVHSFWFTVC/TP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

Met Gln Gly Ile Pro Ile Leu Thr Pro Val Thr Thr Gln Ser Ile Ala  
                   -35                          -30                          -25

Ile Ser Ile Val Leu Thr Val Gln Gly Leu Leu Leu Leu Val His Ser  
       -20                          -15                          -10

Phe Trp Phe Thr Val Cys Thr Pro Val Val Phe  
       -5  1  5

## (2) INFORMATION FOR SEQ ID NO: 512:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq LFCVLLSLRPHTS/GT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

```

Met Gln Asn Phe Cys His His Leu Ala Ile Cys Thr Val Ile Leu Phe
    -25                      -20                      -15

Cys Val Leu Leu Ser Leu Arg Pro His Thr Ser Gly Thr Leu Trp Ala
    -10                      -5                      1                      5

Ser Ser Ala His Gly Leu His Leu Ala Pro Ala Glu Pro Gln Leu Ser
                10                      15                      20

Cys Trp Met Cys Cys Ala
                25

```

## (2) INFORMATION FOR SEQ ID NO: 513:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -64..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq VLMRLVASAYSIA/QK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

```

Met Pro Ser Phe Ser Lys Asp Leu Leu Thr Val Pro Lys Leu Gly Thr
                -60                      -55                      -50

Gly His Xaa Xaa Gly Xaa Gly Ser Tyr Asp Xaa Ala Leu Xaa Leu Leu
                -45                      -40                      -35

Leu Lys Cys Leu Trp Ser Asn Val Val Pro Glu Cys Thr Met Ala Ser
                -30                      -25                      -20

Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr Ser Ile Ala
                -15                      -10                      -5

Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu Gly Asp Leu

```

1                      5                      10                      15  
 Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr Lys Ala Asp  
                     20                      25                      30  
 Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Xaa Xaa Lys Phe Pro  
                     35                      40                      45  
 Lys Leu Xaa Ile Ile Gly Glu Glu Asp Leu Pro Ser Glu Glu Val Asp  
                     50                      55                      60  
 Gln Glu Leu Ile Glu Asp Xaa  
                     65                      70

## (2) INFORMATION FOR SEQ ID NO: 514:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq LEMLXAFASHIXA/RD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu Xaa Ala Phe Ala  
       -20                      -15                      -10  
 Ser His Ile Xaa Ala Arg Asp Ala Ala Gly Ser Gly  
       -5                      1                      5

## (2) INFORMATION FOR SEQ ID NO: 515:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -139..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.2  
seq FGLLHQLSQCVTS/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

Met Glu Val Gly Leu Pro Ala Ile Thr Leu Phe Leu Thr Ser Ala Ser  
-135 -130 -125  
Ser Pro Val Val Ala Thr Thr Met Asp Gln Glu Pro Val Gly Gly Val  
-120 -115 -110  
Glu Arg Gly Glu Ala Val Ala Ala Ser Gly Xaa Ala Ala Ala Ala Ala  
-105 -100 -95  
Phe Gly Glu Ser Ala Gly Gln Met Ser Asn Glu Arg Gly Phe Glu Asn  
-90 -85 -80  
Val Glu Leu Gly Val Ile Gly Lys Lys Lys Lys Val Pro Arg Arg Val  
-75 -70 -65 -60  
Ile His Phe Val Ser Gly Glu Thr Met Glu Glu Tyr Ser Thr Asp Glu  
-55 -50 -45  
Asp Xaa Val Asp Gly Leu Glu Lys Xaa Met Phe Cys Leu Leu Leu Ile  
-40 -35 -30  
Arg Gln Asn Leu Pro Gly Val Pro Thr Tyr Gly Phe Thr Cys Phe Gly  
-25 -20 -15  
Leu Leu His Gln Leu Ser Gln Cys Val Thr Ser Leu Glu  
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -43..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.1  
seq SAATLASLGGTSS/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

Met Lys Glu Leu Glu Arg Gln Gln Lys Glu Val Glu Glu Arg Pro Glu  
                   -40                                  -35                                  -30

Lys Asp Phe Thr Glu Lys Gly Ser Arg Asn Met Pro Gly Leu Ser Ala  
                   -25                                  -20                                  -15

Ala Thr Leu Ala Ser Leu Gly Gly Thr Ser Ser Arg Arg Gly Ser Gly  
                   -10                                  -5                                  1                                  5

Asp Thr Ser Ile Ser Ile Asp Pro Glu  
                                   10

## (2) INFORMATION FOR SEQ ID NO: 517:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1  
seq VLVILCIVTVCVT/IV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Met Ser Met Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile Val  
       -20                                  -15                                  -10

Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu  
       -5                                  1                                  5                                  10

Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala  
                   15                                  20                                  25

Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys  
                   30                                  35                                  40

Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala Val  
       45                                  50                                  55

Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile  
       60                                  65                                  70

## (2) INFORMATION FOR SEQ ID NO: 518:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids

- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -70..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq LLFPLTLVRSFWS/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Met | Glu | Leu | Xaa | Leu | Lys | Xaa | Xaa | Thr | Lys | Xaa | Glu | Xaa | Glu | Ser |  |
| -70 |     |     |     |     | -65 |     |     |     |     | -60 |     |     |     |     | -55 |  |
| Ala | Cys | Thr | Glu | Ala | Tyr | Ser | Gln | Ser | Asp | Glu | Gln | Tyr | Ala | Cys | His |  |
|     |     |     | -50 |     |     |     |     |     | -45 |     |     |     |     | -40 |     |  |
| Leu | Gly | Cys | Gln | Asn | Gln | Leu | Pro | Phe | Ala | Glu | Leu | Arg | Gln | Glu | Gln |  |
|     |     |     | -35 |     |     |     |     | -30 |     |     |     |     | -25 |     |     |  |
| Leu | Met | Ser | Leu | Met | Pro | Lys | Met | His | Leu | Leu | Phe | Pro | Leu | Thr | Leu |  |
|     | -20 |     |     |     |     | -15 |     |     |     |     | -10 |     |     |     |     |  |
| Val | Arg | Ser | Phe | Trp | Ser | Asp | Met | Met | Asp | Ser | Ala | Gln | Ser | Phe | Xaa |  |
| -5  |     |     |     |     | 1   |     |     |     | 5   |     |     |     |     |     | 10  |  |
| Thr | Ser | Ser | Trp | Thr | Phe | Tyr | Leu | Gln | Ala | Asp | Xaa | Gly | Xaa | Ile | Val |  |
|     |     |     | 15  |     |     |     |     | 20  |     |     |     |     |     | 25  |     |  |
| Ile | Xaa | Gln | Ser | Lys | Pro | Glu | Ile | Gln | Tyr | Ala | Pro | His | Leu | Glu | Gln |  |
|     |     | 30  |     |     |     |     | 35  |     |     |     |     |     | 40  |     |     |  |
| Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6  
seq GLILLFASHLINQ/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

Met Val Ser Asn Ala Ser Glu Thr Ser Cys Leu Gly Leu Ile Leu Leu  
-20 -15 -10

Phe Ala Ser His Leu Ile Asn Gln Phe Ser Ser  
-5 1

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -73..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6  
seq LIVFISVCTALLA/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu  
-70 -65 -60

Leu Leu Gly Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe  
-55 -50 -45

Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg  
-40 -35 -30

Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe  
-25 -20 -15 -10

Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu  
-5 1 5

Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys  
10 15 20

Gln Ser Lys Lys Tyr Leu Met Val Glu Trp Trp Gln Xaa Phe Leu Phe  
25 30 35

Tyr Pro Ser Phe Leu Xaa Pro Lys Xaa Val Ser Ser  
40 45 50

## (2) INFORMATION FOR SEQ ID NO: 521:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq LGAAALALLLANT/DV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

Met Gly Met Trp Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu  
                  -20                  -15                  -10

Ala Leu Leu Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys  
                  -5                                  1                                  5

Ala Ala Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys  
10                                  15                                  20                                  25

Glu Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala  
                                  30                                  35                                  40

Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu  
                  45                                  50                                  55

Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val  
                  60                                  65                                  70

Pro Leu Tyr Ala Val Val Lys Glu Gln Arg  
75                                  80

## (2) INFORMATION FOR SEQ ID NO: 522:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate



## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq LPLLLVANAGTAA/VG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

```

Met Asp Val Ala Phe Leu Glu Xaa Leu Ile Lys Asp Asp Ile Glu Arg
  -30                      -25                      -20

Gly Arg Leu Pro Leu Leu Leu Val Ala Asn Ala Gly Thr Ala Ala Val
-15                      -10                      -5                      1

Gly His Thr Asp Lys Ile Gly Arg Leu Lys Glu Leu Cys Glu Gln Tyr
              5                      10                      15

Gly Ile Trp Leu His Val Glu Gly Val Asn
      20                      25

```

## (2) INFORMATION FOR SEQ ID NO: 523:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq LFNLLWLALACSP/VW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

```

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
  -15                      -10                      -5

Val Trp
  1

```

## (2) INFORMATION FOR SEQ ID NO: 524:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -33..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.8  
seq FICLQWALPHSEA/GD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

Met Asn Ala Gln Pro Gly Leu Xaa Leu Asp Cys Ile Thr Arg Phe Leu  
-30 -25 -20

Thr Xaa Gly Gln Phe Ile Cys Leu Gln Trp Ala Leu Pro His Ser Glu  
-15 -10 -5

Ala Gly Asp Phe Glu Ala Lys  
1 5

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -69..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7  
seq LCRLCLVRLFCC/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

Met Gly Lys Glu Trp Gly Trp Gln Glu Met Glu Asn Gly Gly Ala Ala  
-65 -60 -55

Pro Ala Trp Gly Ala Gly Pro Pro Val His Pro Ala Pro Pro Val  
-50 -45 -40

Glu Lys Thr Leu Ser Trp Gly Cys Gly Phe Gly Leu His Ser Gly Phe  
-35 -30 -25

Gly Gly Ser Gly Gly Gly Val Gly Leu Cys Arg Leu Leu Cys Leu Val

-20

-15

-10

Arg Leu Phe Cys Cys Ser Ser Ile Leu Tyr Gln Arg Gln Lys  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 526:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq AALLLTATVRLSA/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Met Ala Ala Pro Ser Gly Gly Trp Asn Gly Val Gly Ala Ser Leu Trp  
-25 -20 -15

Ala Ala Leu Leu Leu Thr Ala Thr Val Arg Leu Ser Ala Ser Pro Gly  
-10 -5 1

Pro

## (2) INFORMATION FOR SEQ ID NO: 527:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq LLLFFGKLLVGG/VG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -91..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.7  
seq SVLELIVASVCQS/HI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

Met Glu Arg Asn Cys Lys Gly Ser Phe Gly Val Ile Lys Glu Gly Asp  
-90 -85 -80

Thr Asp Thr Xaa Glu Thr Lys Ala Arg Arg Thr Val Trp Glu Pro Arg  
-75 -70 -65 -60

Gly Arg Tyr Ser Phe Arg Xaa Thr Pro Arg Pro Ala Tyr Pro Val Glu  
-55 -50 -45

Gln Cys Gly Phe Ala Arg Arg Ala Leu Glu Leu Leu Glu Ile Arg Lys  
                   -40                                  -35                                  -30

His Ser Pro Glu Val Cys Glu Pro Pro Asn Ile Pro Val Thr Ser Val  
                   -25                                  -20                                  -15

Leu Glu Leu Ile Val Ala Ser Val Cys Gln Ser His Ile Arg Thr Thr  
                   -10                                  -5                                  1                                  5

## (2) INFORMATION FOR SEQ ID NO: 529:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -66..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq LYMLAEALPVSHG/AH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

Met Phe Val Glu Tyr Arg Lys Gln Leu Lys Leu Leu Leu Asp Arg Leu  
      -65                                  -60                                  -55

Ala Gln Val Ser Pro Glu Leu Leu Leu Ala Ser Val Arg Arg Val Phe  
      -50                                  -45                                  -40                                  -35

Ser Ser Thr Leu Gln Asn Trp Gln Thr Thr Arg Phe Met Glu Val Glu  
                   -30                                  -25                                  -20

Val Ala Ile Arg Leu Leu Tyr Met Leu Ala Glu Ala Leu Pro Val Ser  
                   -15                                  -10                                  -5

His Gly Ala His Phe Ser Gly Asp Val Ser Lys Ala Ser Ala Leu Gln  
                   1                                  5                                  10

Asp Met Met Arg Thr Leu Val Thr Ser Gly Val Ser Gly  
      15                                  20                                  25

## (2) INFORMATION FOR SEQ ID NO: 530:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -21..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7

seq IIFLIQWHGVSFQ/EF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

Met Leu Leu Gly Thr Ser Asn Ile Ile Ile Phe Leu Ile Gln Trp His  
-20 -15 -10

Gly Ser Val Phe Gln Glu Phe  
-5 1

(2) INFORMATION FOR SEQ ID NO: 531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -20..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.6

seq AFVXACVLSLIST/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Xaa Asn Arg Phe Ala Thr Ala Phe Val Xaa Ala Cys Val Leu Ser  
-20 -15 -10 -5

Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp  
1 5 10

Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys  
15 20 25

Ser Ile Trp Asp Glu Leu  
30

## (2) INFORMATION FOR SEQ ID NO: 532:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq MSLTSGFLRVSQG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

Met Ser Leu Thr Ser Gly Phe Leu Arg Val Ser Gln Gly Ser Pro Asn  
-10 -5 1

Leu Ser Gln  
5

## (2) INFORMATION FOR SEQ ID NO: 533:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -63..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq AIRTLFSVTGILA/EQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

Met Ala Asn Phe Lys Gly His Ala Leu Pro Gly Ser Phe Phe Leu Ile  
-60 -55 -50

Ile Gly Leu Cys Trp Ser Val Lys Tyr Pro Leu Lys Tyr Phe Ser His  
-45 -40 -35

```

Thr Arg Lys Asn Ser Pro Leu His Tyr Tyr Gln Arg Leu Glu Ile Val
-30                               -25                               -20

Glu Ala Ala Ile Arg Thr Leu Phe Ser Val Thr Gly Ile Leu Ala Glu
-15                               -10                               -5                               1

Gln Phe Val Pro Asp Gly Pro His Leu His Leu Tyr His Glu Asn His
                    5                               10                               15

Trp Ile Lys Leu Met Asn
                20

```

## (2) INFORMATION FOR SEQ ID NO: 534:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq AGLLFGSLAGLGA/YQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

```

Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly
-50                               -45                               -40

Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala
-35                               -30                               -25

Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala
-20                               -15                               -10                               -5

Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val
                1                               5                               10

Phe Leu Ala Thr Ser Gly Thr Leu Ala
                15                               20

```

## (2) INFORMATION FOR SEQ ID NO: 535:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -35..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.4  
seq CCALLTSLXCIWG/PA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

```

Met Glu Xaa Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly Tyr
-35          -30          -25          -20

Thr Xaa Xaa Xaa Xaa Tyr Cys Cys Ala Leu Leu Thr Ser Leu Xaa Cys
          -15          -10          -5

Ile Trp Gly Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys
      1          5          10

```

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -42..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.4  
seq ITGVILLAVGIWG/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

```

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
      -40          -35          -30

Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
      -25          -20          -15

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
      -10          -5          1          5

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
      10          15          20

```

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Leu  
           25                                  30                                  35

## (2) INFORMATION FOR SEQ ID NO: 537:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -67..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq LSVSLLPCAGAWS/LL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

Met Phe Ser Arg Glu Leu Ala Pro Thr Arg Ile Gly Gly Ala Ser Ser  
           -65                                  -60                                  -55

Gly Ser Arg Ser Gly Gly Thr Leu Ile Ser Thr Ala Pro Leu Thr Thr  
           -50                                  -45                                  -40

Arg Val Leu Asn Pro Thr Ala Gln Cys Phe Cys Leu Asp Cys Thr Leu  
           -35                                  -30                                  -25                                  -20

Arg Arg Met Gln Thr His Leu Ser Val Ser Leu Leu Pro Cys Ala Gly  
                                   -15                                  -10                                  -5

Ala Trp Ser Leu Leu Xaa Ser Lys Lys Val Ile Leu Pro Ser Cys Ser  
                                   1                                  5                                  10

Ser Ile Leu Xaa Thr Val Val Val Ile  
           15                                  20

## (2) INFORMATION FOR SEQ ID NO: 538:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq LLMLGVTL PNSYW/RV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

```

Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe Met Ala Thr Val Gly
      -25                      -20                      -15
Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg Val Ser
      -10                      -5                      1
Thr Val His Gly Asn Val Ile Xaa Thr Asn Xaa Ile Phe Glu Asn Leu
      5                      10                      15
Trp Phe Ser Ser Ala Gly
20                      25

```

## (2) INFORMATION FOR SEQ ID NO: 539:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq XFLXLXXLSXXWP/XD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

```

Met Glu Lys Ile Pro Val Ser Xaa Phe Leu Xaa Leu Xaa Xaa Leu Ser
-20                      -15                      -10                      -5
Xaa Xaa Trp Pro Xaa Asp Thr Thr Val Lys Pro Gly Ala Xaa Lys Asp
      1                      5                      10
Thr Lys Asp Ser Arg Xaa Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
      15                      20                      25
Gly Asp Gln Leu Ile Trp Thr Arg
30                      35

```

## (2) INFORMATION FOR SEQ ID NO: 540:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -67..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq LILERPLVPSAEA/SG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

Met His Ser Ala Glu Glu Pro Leu Xaa Leu Ala Ala Leu Arg Gly Ala  
-65 -60 -55

Arg Gly His Leu Pro Cys Gly Ser Arg His His Val Gly Ser Leu Ala  
-50 -45 -40

Pro Ala Ser Val Pro Ala Pro Gly Ala Cys Leu Trp Val Cys Glu Trp  
-35 -30 -25 -20

Glu Thr Leu Leu Pro Gly Leu Ile Leu Glu Arg Pro Leu Val Pro Ser  
-15 -10 -5

Ala Glu Ala Ser Gly Ala Gly Lys Leu Ser Arg Lys Glu Ala Leu Leu  
1 5 10

Ser Asn Tyr Ala Leu  
15

## (2) INFORMATION FOR SEQ ID NO: 541:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.9  
seq GLWLALVDGLVRX/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

```

Met Ala Gly Gln Phe Arg Ser Tyr Val Trp Asp Pro Leu Leu Ile Leu
    -40                      -35                      -30

Ser Gln Ile Val Leu Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu
    -25                      -20                      -15

Trp Leu Ala Leu Val Asp Gly Leu Val Arg Xaa Ala Pro Arg Trp Ile
    -10                      -5                      1                      5

Xaa Gly

```

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -78..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq VGAVFGLTTCISA/HV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

```

Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr
    -75                      -70                      -65

Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala
    -60                      -55                      -50

Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
    -45                      -40                      -35

Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
    -30                      -25                      -20                      -15

Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
    -10                      -5                      1

Arg Glu Lys Pro Asp Asp Pro Leu Asn Arg
    5                      10

```

## (2) INFORMATION FOR SEQ ID NO: 543:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq WLQVLPVILLLLG/VP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu  
-15 -10 -5

Leu Gly Val Pro Pro Ser  
1

## (2) INFORMATION FOR SEQ ID NO: 544:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq LLILDMNVLYTDA/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

Met Glu Ile Tyr Phe Ile Phe Cys Ile Ile Val Pro Ile Ala Ala Ala  
-35 -30 -25

Thr Val Tyr Lys Ser Trp Cys Leu Leu Leu Ile Leu Asp Met Asn Val  
-20 -15 -10

Leu Tyr Thr Asp Ala Ser Pro Leu Gly  
-5 1

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq VLLAIGMFFTAWF/FV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala Val Phe Pro His Leu  
-30 -25 -20

Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr Ala Trp Phe Phe  
-15 -10 -5 1

Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg Asp Ile Tyr Lys Glu  
5 10 15

Leu Gln

(2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq LMLSSSLPLLIWL/KD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

```

Met Arg Leu Ala Ala Glu Ala His Pro Gly Arg Thr His Thr Leu Phe
-35                -30                -25                -20

Arg Arg Leu Lys Pro Phe Leu Met Leu Ser Ser Ser Leu Pro Leu Leu
          -15                -10                -5

Ile Trp Leu Lys Asp Arg
          1

```

(2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq IILFSAIVGFIYG/YV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

```

Met Leu Glu His Leu Xaa Ser Leu Pro Thr Gln Met Asp Tyr Lys Gly
          -35                -30                -25

Gln Lys Leu Ala Xaa Gln Met Phe Gln Gly Ile Ile Leu Phe Ser Ala
          -20                -15                -10

Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr
          -5                1                5

Val Tyr Ile Val Met Ala Gly
10                15

```

(2) INFORMATION FOR SEQ ID NO: 548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:



(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -16..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.8  
seq SKVLFCFSNVLG/FD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

Met Glu Tyr Ser Lys Val Leu Phe Cys Ser Phe Ser Asn Val Leu Gly  
-15 -10 -5

Phe Asp Tyr  
1

## (2) INFORMATION FOR SEQ ID NO: 549:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -26..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.7  
seq LIMQLGSVLLTRC/PF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met  
-25 -20 -15

Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe  
-10 -5 1 5

Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro  
10 15 20

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Ser Gly  
25 30

## (2) INFORMATION FOR SEQ ID NO: 550:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq LGLALGRLEGGSA/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala Pro Ser  
-50 -45 -40

Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val Arg Asp  
-35 -30 -25

Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg Leu Glu  
-20 -15 -10 -5

Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg Ala Ala  
1 5 10

Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val Pro  
15 20 25

(2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq LIALTCLDGTTVS/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

Met Asn Ala Leu Met Val Leu Phe Asn Val Thr Val Val Leu Ile Ala

-25                      -20                      -15  
 Leu Thr Cys Leu Asp Gly Thr Thr Val Ser Ala Glu Met Ala Thr Met  
 -10                      -5                      1                      5  
 Thr Met Gly Cys Phe His Gln Val Glu Asn Arg Val Lys Ile Leu Met  
                     10                      15                      20  
 Ser Val Gly Pro Gly Gly Thr Ala Val Pro Met Ile Pro Phe Ala Ser  
                     25                      30                      35  
 Ile Trp Met Ala Asp Met Ile Xaa Asp  
                     40                      45

## (2) INFORMATION FOR SEQ ID NO: 552:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -45..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq VLVYLVTAERVWS/DD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr  
 -45                      -40                      -35                      -30  
 Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg  
                     -25                      -20                      -15  
 Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His  
                     -10                      -5                      1  
 Lys

## (2) INFORMATION FOR SEQ ID NO: 553:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -16..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.5  
seq SLFIYIFXTCSNT/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Xaa Thr Cys Ser Asn Thr  
-15 -10 -5  
Ser Pro Ser Tyr Gln Xaa Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala  
1 5 10 15  
Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe  
20 25 30  
Cys Phe Xaa Leu Gln  
35

## (2) INFORMATION FOR SEQ ID NO: 554:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -16..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq LNSLSALAEAVG/SR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly  
-15 -10 -5  
Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Arg Arg  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO: 555:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 44 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -17..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 4.4  
                            seq TLRTWLCCAGSWA/VE
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

Met Thr Ala Gly Thr Leu Arg Thr Trp Leu Cys Cys Ala Gly Ser Trp  
      -15                      -10                      -5

Ala Val Glu Leu Pro Ala Glu Pro Leu Val Val Phe Cys Xaa Ser Thr  
      1                      5                      10                      15

Ser Arg Lys Arg Ala Lys Gly Leu Ile Gln Ser Val  
          20                      25

(2) INFORMATION FOR SEQ ID NO: 556:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 26 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -24..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 4.3  
                            seq RLLVILCVSVKAG/ST
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

Met Leu Gly Arg Pro Cys Phe His Ser Pro Gln Arg Leu Leu Val Ile  
      -20                      -15                      -10

Leu Cys Val Ser Val Lys Ala Gly Ser Thr  
      -5                      1

## (2) INFORMATION FOR SEQ ID NO: 557:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq LQFVLPVATQIQQ/EV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

Met Asp Glu Ala Arg Asp Asn Ala Cys Asn Asp Met Gly Lys Met Leu  
-25 -20 -15

Gln Phe Val Leu Pro Val Ala Thr Gln Ile Gln Gln Glu Val Ile Lys  
-10 -5 1

## (2) INFORMATION FOR SEQ ID NO: 558:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq LCALGSAPSSMWA/GE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

Met Ser Pro Ile Ser Ile Arg Glu Leu Cys Ala Leu Gly Ser Ala Pro  
-20 -15 -10

Ser Ser Met Trp Ala Gly Glu  
-5 1

## (2) INFORMATION FOR SEQ ID NO: 559:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq MTDLLSASPWALT/IV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

Met Thr Asp Leu Leu Ser Ala Ser Pro Trp Ala Leu Thr Ile Val Ser  
-10 -5 1

Ser Glu Leu His Leu Ala Pro Ser Met Thr Thr Val Asp Gln Leu Glu  
5 10 15

Ser Gln Val Asp Asn Val Ile Leu Gln Thr Gly Glu Ser Ala Ser Glu  
20 25 30 35

Cys Phe Cys Leu Gln Cys Pro Ser Leu Gly Asn Ile Glu Gly Gly Val  
40 45 50

Ala Thr Gly His Xaa  
55

## (2) INFORMATION FOR SEQ ID NO: 560:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2

seq LTCGPALVPRLWA/TC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

Met Ser Trp Ser Gly Leu Leu His Gly Leu Asn Thr Ser Leu Thr Cys  
 -25 -20 -15

Gly Pro Ala Leu Val Pro Arg Leu Trp Ala Thr Cys Ser Met Ala Thr  
 -10 -5 1 5

Leu Asn Gln Met His Arg Leu Gly Pro Pro Lys Arg Pro Pro Arg Lys  
 10 15 20

Leu Gly Pro Thr Glu Gly Arg Pro Gln Leu Lys Gly Val Val Leu Cys  
 25 30 35

Thr Phe Thr Arg Asn Arg  
 40

(2) INFORMATION FOR SEQ ID NO: 561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq LEAFSQAISAIQA/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

Met Ala Asp Val Ile Asn Val Ser Val Asn Leu Glu Ala Phe Ser Gln  
 -20 -15 -10

Ala Ile Ser Ala Ile Gln Ala Leu Arg Ser Ser Val Ser Arg Val Phe  
 -5 1 5

Asp Cys Leu Lys Asp Gly Met Arg Asn Lys Glu Thr Leu Glu Gly Arg  
 10 15 20 25

Glu Lys Ala Phe Ile Ala His Phe Gln Asp Asn Leu His Ser Val Asn  
 30 35 40

Arg Asp Pro



## (2) INFORMATION FOR SEQ ID NO: 562:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq RLLSSLLLTMSNN/NP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu His  
-30 -25 -20

Ser Asn Val Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn Asn  
-15 -10 -5

Asn Pro Glu Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val Tyr  
1 5 10 15

His Ala Asp Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val Ser  
20 25 30

Lys Tyr Thr Met Ala Leu Gln Gln Lys Lys Ala Leu Ser  
35 40 45

## (2) INFORMATION FOR SEQ ID NO: 563:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq ACLAWTAVRPSAC/CH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

Met Thr Ser Ala Cys Leu Ala Trp Thr Ala Val Arg Pro Ser Ala Cys  
 -15 -10 -5

Cys His Pro Gln Ser Ala Asn Trp  
 1 5

## (2) INFORMATION FOR SEQ ID NO: 564:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq VFGMSSSSGASNS/AP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Met Asn Gly Ser Arg Thr Leu Thr His Ser Ile Ser Asp Gly Gln Leu  
 -55 -50 -45 -40

Gln Gly Gly Gln Ser Asn Ser Glu Leu Phe Gln Gln Glu Xaa Gln Thr  
 -35 -30 -25

Ala Pro Ala Gln Val Pro Gln Gly Phe Asn Val Phe Gly Met Ser Ser  
 -20 -15 -10

Ser Ser Gly Ala Ser Asn Ser Ala Pro His Leu Gly Phe His Leu Gly  
 -5 1 5

Ser Lys Gly Thr Ser Ser Leu Ser Gln Gln Thr Pro Gly  
 10 15 20

## (2) INFORMATION FOR SEQ ID NO: 565:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq FFLFLSFVLMYDG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

```

Met Leu Gly Phe Phe Leu Phe Leu Ser Phe Val Leu Met Tyr Asp Gly
-15                -10                -5

Leu Arg Leu Phe Gly Ile Leu Ser Thr Cys Arg Val His His Thr Met
 1              5              10              15

Asn Gln Phe Leu Ile Asp Ile Ser Ser Phe Thr Ser Arg Val Arg
      20              25              30

```

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq SIKVLLQSALSLG/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

```

Met Met Glu Glu Arg Ala Asn Leu Met His Met Met Lys Leu Ser Ile
-25                -20                -15

Lys Val Leu Leu Gln Ser Ala Leu Ser Leu Gly Arg Ser Leu Asp Ala
-10              -5              1              5

Asp His Ala Pro Leu Gln Gln Phe Phe Val Val Met Glu His Cys Ser
      10              15              20

```

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids

- (B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -17..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.9  
seq XIVSAALLAFVQT/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

Met Glu Leu Glu Xaa Ile Val Ser Ala Ala Leu Leu Ala Phe Val Gln  
-15 -10 -5  
Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp Glu Val Ile Phe  
1 5 10 15  
Ser Tyr Val Xaa Gly Val Leu Glu Asp Leu Gly Pro Ser Gly Pro Ser  
20 25 30  
Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met Met Glu Ala Xaa  
35 40 45  
Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile Gly Xaa Met Met  
50 55 60

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -26..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.9  
seq SLIPLFXFIGTGA/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

Met Leu Arg Gln Ile Ile Gly Gln Ala Lys Lys His Pro Ser Leu Ile  
-25 -20 -15

Pro Leu Phe Xaa Phe Ile Gly Thr Gly Ala Thr Gly Ala Thr Leu Tyr  
 -10                               -5                               1                               5

Leu Leu Arg Leu Ala Leu Phe Asn Pro Xaa Val Cys Trp Asp Arg Xaa  
                   10                               15                               20

Asn Pro Glu Pro Trp Asn Xaa Leu Gly Pro Glu  
                   25                               30

## (2) INFORMATION FOR SEQ ID NO: 569:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -98..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.8  
   seq WTSLTCSLVVVDG/CG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Met Val Lys Glu Thr Gln Tyr Tyr Asp Ile Leu Gly Val Lys Pro Ser  
                   -95                               -90                               -85

Ala Ser Pro Glu Arg Ser Arg Arg Pro Ile Gly Ser Trp Arg Ser Ser  
                   -80                               -75                               -70

Thr Thr Arg Thr Arg Thr Arg Met Arg Ala Arg Ser Leu Asn Ser Tyr  
                   -65                               -60                               -55

Pro Arg His Met Lys Cys Phe Gln Ile Gln Arg Lys Gly Met Phe Met  
                   -50                               -45                               -40                               -35

Thr Lys Ala Glu Ser Arg Gln Xaa Lys Lys Glu Ala Gln Ala Ala Pro  
                   -30                               -25                               -20

Ala Ser Leu His Pro Trp Thr Ser Leu Thr Cys Ser Leu Val Val Val  
                   -15                               -10                               -5

Asp Gly Cys Gly  
                   1

## (2) INFORMATION FOR SEQ ID NO: 570:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq RALSTXLFGSIRG/AA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

```

Met Ala Asn Leu Phe Ile Arg Lys Met Val Asn Pro Leu Leu Tyr Leu
-35                -30                -25

Ser Arg His Thr Val Lys Pro Arg Ala Leu Ser Thr Xaa Leu Phe Gly
-20                -15                -10                -5

Ser Ile Arg Gly Ala Ala Pro Val Ala Val Glu Pro Gly Ala Ala Val
                1                5                10

Arg Ser Leu Leu Ser Pro Gly Leu Leu Pro His Leu Leu Pro Ala Leu
        15                20                25

Gly Phe Lys Asn Lys Thr Val Leu Lys Lys Arg Cys Lys Asp Cys Tyr
        30                35                40

Leu Val Lys Arg Arg Gly Arg Trp Tyr Val Tyr Cys Lys Thr His Pro
        45                50                55                60

Arg His Lys Gln Arg His Met Xaa Thr Leu Ser Leu Gln Ser His Ala
        65                70                75

Gln -
```

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq RIHLCQRSPGSQG/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

Met Ala Ala Ala Ala Ser Arg Gly Xaa Gly Ala Lys Leu Gly Leu  
           -30                              -25                              -20  
 Arg Xaa Ile Arg Ile His Leu Cys Gln Arg Ser Pro Gly Ser Gln Gly  
           -15                              -10                              -5  
 Val Arg Asp Phe Ile  
       1  5

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -44..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
                               seq IALTLIPSMLSRA/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

Met Phe Pro Ser Cys Tyr Leu Cys Tyr Ser Leu Cys Gly Ser Ile Leu  
                               -40                              -35                              -30  
 Leu Ser Ile Phe Ser Ala Tyr Asn Arg Leu Ser Leu Met Leu Arg Ile  
                               -25                              -20                              -15  
 Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala Ala Gly Trp Cys  
           -10                              -5  1  
 Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu Cys Leu Pro Cys  
       5  10  15  20  
 Gly

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq QLXFLYFVCCIFQ/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

```

Met Ser Thr Gln Xaa Gly Leu Ser Met His Ala His Pro Gln Ala Tyr
-60                               -55                               -50                               -45

Thr Pro Phe Ile Tyr Leu His Ala Arg Lys Arg Arg Gly Glu Ile Gly
-40                               -35                               -30

Asp Ala Asp Ser Arg Phe Asn Asp Arg Tyr Ala His Lys Ser Ala Gln
-25                               -20                               -15

Leu Xaa Phe Leu Tyr Phe Val Cys Cys Ile Phe Gln Asp Val Tyr Tyr
-10                               -5                               1

Xaa
5

```

(2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq SSCSCSLISFTRG/DK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

```

Met Lys His Phe Gln Asp Leu Pro Ser Ser Cys Ser Cys Ser Leu Ile
-20                               -15                               -10

```



Ser Phe Thr Arg Gly Asp Lys Tyr Phe Ala Tyr Asn Glu Glu Ile Phe  
 -5 1 5 10  
 Leu Val Tyr Asn Ala Asp Gln  
 15

## (2) INFORMATION FOR SEQ ID NO: 575:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -62..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq SILGIISVPLSIG/YC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

Met Ser Gln Arg Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr Arg  
 -60 -55 -50  
 Xaa Leu Ile Glu Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys  
 -45 -40 -35  
 Val Leu Pro His Met Ile Glu Arg Lys Xaa Xaa Lys Ile Val Thr Val  
 -30 -25 -20 -15  
 Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys  
 -10 -5 1  
 Ala Ser Xaa His Ala Leu Xaa Gly Phe Phe Asn Xaa Leu Arg Thr Xaa  
 5 10 15  
 Leu Ala Thr Tyr Pro Gly Ile Ile Val Ser  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 576:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -98..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq LALRTSWISSVCS/VT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

```

Met Gly Gly Ser Gly Ser Arg Leu Ser Lys Glu Leu Leu Ala Glu Tyr
      -95                      -90                      -85

Gln Asp Leu Thr Phe Leu Thr Lys Gln Glu Ile Leu Leu Ala His Arg
      -80                      -75                      -70

Arg Phe Cys Glu Leu Leu Pro Gln Glu Gln Arg Xaa Xaa Ser Arg His
      -65                      -60                      -55

Phe Gly His Lys Cys Pro Ser Ser Arg Phe Ser Ala Phe Gln Ser Ser
      -50                      -45                      -40                      -35

Arg Pro Thr Pro Ser Arg Ser Glu Ser Ala Gly Ser Ser Pro His Pro
      -30                      -25                      -20

Gln Pro Lys Thr Ala Leu Ala Leu Arg Thr Ser Trp Ile Ser Ser Val
      -15                      -10                      -5

Cys Ser Val Thr Gln Pro Arg Gln Thr Ser Ser Pro Ile Met Pro Ser
      1                      5                      10

Ala Ser Leu Thr Leu Met Met Thr
      15                      20

```

## (2) INFORMATION FOR SEQ ID NO: 577:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq PLSDSWALLPASA/GV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro  
                   -25                  -20                  -15

Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr  
                   -10                  -5                  1

Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro  
   5                  10                  15                  20

Lys Leu Leu

## (2) INFORMATION FOR SEQ ID NO: 578:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -114..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq ATFVTQALIQXYA/RI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

Met Ala Asp His Val Gln Ser Leu Ala Gln Leu Glu Asn Leu Cys Lys  
                   -110                  -105                  -100

Gln Leu Tyr Glu Thr Thr Asp Thr Xaa Xaa Arg Ser Ser Xaa Ala Glu  
                   -95                  -90                  -85

Lys Ala Leu Val Glu Phe Thr Asn Ser Pro Asp Cys Leu Ser Lys Cys  
                   -80                  -75                  -70

Gln Leu Leu Leu Glu Arg Gly Ser Ser Ser Tyr Ser Gln Leu Leu Ala  
                   -65                  -60                  -55

Ala Thr Cys Leu Thr Lys Leu Val Ser Arg Thr Asn Asn Pro Leu Pro  
                   -50                  -45                  -40                  -35

Leu Glu Gln Arg Ile Asp Ile Arg Asn Tyr Val Leu Asn Xaa Leu Ala  
                   -30                  -25                  -20

Thr Arg Pro Lys Leu Ala Thr Phe Val Thr Gln Ala Leu Ile Gln Xaa  
                   -15                  -10                  -5

Tyr Ala Arg Ile Thr Lys Leu Gly Trp Phe Asp  
                   1                  5

## (2) INFORMATION FOR SEQ ID NO: 579:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq TCSVCCYLFWLIA/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

Met Ala Tyr His Gly Leu Thr Val Pro Leu Ile Val Met Ser Val Phe  
-55 -50 -45 -40

Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly Pro  
-35 -30 -25

Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Cys  
-20 -15 -10

Tyr Leu Phe Trp Leu Ile Ala Ile Pro Ala Trp  
-5 1

## (2) INFORMATION FOR SEQ ID NO: 580:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -58..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq GGILMGSFQGTIA/GQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

```

Met Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His
      -55                -50                -45

Ser Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu
      -40                -35                -30

Ile Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile
      -25                -20                -15

Leu Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala
-10                -5                1                5

Thr Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly
      10                15                20

Ala Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ser
      25                30                35

His Pro Ala Leu Ala Ala Thr Ala Phe Ser Leu Xaa Cys Pro Arg Gly
      40                45                50

Val Gln Xaa Leu Met Ile Ser Ile Ser Glu His Leu Phe Ile His Ala
55                60                65                70

```

## (2) INFORMATION FOR SEQ ID NO: 581:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq RWWCFHLQAEASA/HP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

```

Met Gly Trp Gln Arg Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser
      -15                -10                -5

Ala His Pro Pro Gln Gly Leu Gln
      1                5

```

## (2) INFORMATION FOR SEQ ID NO: 582:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq VIFFACVVRVRDG/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

```

Met Ser Val Ile Phe Phe Ala Cys Val Val Arg Val Arg Asp Gly Leu
-15                -10                -5                1

Pro Leu Ser Ala Ser Thr Asp Phe Tyr His Thr Gln Asp Phe Leu Glu
          5                10                15

Trp Arg Arg Arg Leu Lys Ser Leu Ala Leu Arg Leu Lys
    20                25                30

```

## (2) INFORMATION FOR SEQ ID NO: 583:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq TALAAXTWLGWVG/VR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

```

Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp Gly
-15                -10                -5

Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu Asn
  1                5                10                15

```

Xaa Arg Glu Gln Ala Glu Xaa Xaa Arg Tyr Phe  
35 40

```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
```

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 12  
seq FTLFLALIGGTSG/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:

Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr  
-15 -10 -5Ser Gly Gln Tyr Tyr Asp Trp  
1 5

(2) INFORMATION FOR SEQ ID NO: 586:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -18..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 12  
seq FTLFLALIGGTSG/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:

Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr  
-15 -10 -5Ser Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln  
1 5 10Ser Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro  
15 20 25 30Ser Ala Met Tyr Cys Asp Glu Leu Lys Leu Lys Ser Val Pro Met Val  
35 40 45Pro Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His  
50 55 60Ile Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO: 587:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 111 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.9  
seq LLLLLLPFLLYMA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

```
Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Pro Phe Leu
-20          -15          -10          -5

Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
          1              5              10

Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
          15              20              25

Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
          30              35              40

Gly Ala Arg Val Tyr Xaa Ala Xaa Xaa Asp Val Glu Lys Gly Glu Leu
          45              50              55              60

Val Ala Xaa Glu Ile Gln Thr Thr Thr Gly Xaa Xaa Gln Val Leu Val
          65              70              75

Arg Xaa Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala
          80              85              90
```

(2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1

seq LLYLLVPALFCRA/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

Met Trp Leu Leu Tyr Leu Leu Val Pro Ala Leu Phe Cys Arg Ala Gly  
 -15 -10 -5 1

Gly Ser Ile Pro Ile Pro Gln Lys Leu Phe Gly Glu Val Thr Ser Pro  
 5 10 15

Leu Phe Pro Lys Pro Tyr Pro Asn Gly  
 20 25

(2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7  
seq LLFLVAGLLPSFP/AN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

Met Lys Gln Ile Leu His Pro Ala Leu Glu Thr Thr Ala Met Thr Leu  
 -30 -25 -20

Phe Pro Val Leu Leu Phe Leu Val Ala Gly Leu Leu Pro Ser Phe Pro  
 -15 -10 -5

Ala Asn Glu Asp Lys Asp Pro Ala Phe Thr Ala Leu Leu Thr Thr Gln  
 1 5 10 15

Thr Gln Val Gln Arg Glu Ile Val Asn Lys His Asn Glu Leu Arg Arg  
 20 25 30

Ala Val Ser Pro Pro Ala Lys  
 35

(2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -17..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.9  
seq LFLTMLTLALVKS/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

```
Met Leu Lys Ala Leu Phe Leu Thr Met Leu Thr Leu Ala Leu Val Lys
   -15                      -10                      -5

Ser Gln Asp Thr Glu Glu Thr Ile Thr Tyr Thr Gln Cys Thr Asp Gly
   1                      5                      10                      15

Tyr Glu Trp Asp Pro Val Arg Gln Gln Cys Lys Asp Ile Asp Glu Cys
   20                      25                      30

Asp Ile Val Pro Asp Ala Cys Lys Gly Gly Met Lys Cys Val Asn His
   35                      40                      45

Tyr Gly Gly Tyr Leu Cys Leu Pro Lys Thr Ala Gln Ile Ile Val Asn
   50                      55                      60

Asn Glu Gln Pro Gln Gln Glu Thr Gln Pro Ala Glu Gly Thr Ser Gly
   65                      70                      75

Ala Thr Thr Gly Val Val Ala Ala Xaa Ser Met Ala Thr Ser Xaa Val
   80                      85                      90                      95

Leu Xaa Gly Gly Gly Phe Val Ala Ser Ala Ala Ala Val Ala Gly Pro
   100                     105                     110

Glu Met Gln Thr Gly Arg Asn Asn Phe Val
   115                      120
```

(2) INFORMATION FOR SEQ ID NO: 591:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -22..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.9  
 seq LLILWFHLDCVSS/IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

Met Glu Lys Asn Pro Leu Ala Ala Pro Leu Leu Ile Leu Trp Phe His  
 -20 -15 -10  
 Leu Asp Cys Val Ser Ser Ile Leu Asn Val Glu Gln Ser Pro Gln Ser  
 -5 1 5 10  
 Leu His Val Gln Glu Gly Asp Ser Thr Asn Phe Thr Cys Ser Phe Pro  
 15 20 25  
 Ser Ser Asn Phe Tyr Ala Leu His Trp Tyr Arg Trp Glu Thr Ala Lys  
 30 35 40  
 Ser Pro Glu Ala Val  
 45

(2) INFORMATION FOR SEQ ID NO: 592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -15..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.3  
 seq VVTIVILLCFCKA/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

Met Arg Val Val Thr Ile Val Ile Leu Leu Cys Phe Cys Lys Ala Ala  
 -15 -10 -5 1  
 Glu Leu Arg Lys Ala Ser Pro Gly Ser Val Arg Ser Arg Val Asn His  
 5 10 15  
 Gly Arg Ala Gly Gly  
 20

(2) INFORMATION FOR SEQ ID NO: 593:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -90..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq LLFVATLPFWTHY/LI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

Met Asp Gln Phe Pro Glu Ser Val Thr Glu Asn Phe Glu Tyr Asp Asp  
-90 -85 -80 -75

Leu Ala Glu Ala Cys Tyr Ile Gly Asp Ile Val Val Phe Gly Thr Val  
-70 -65 -60

Phe Leu Ser Ile Phe Tyr Ser Val Ile Phe Ala Ile Gly Leu Val Gly  
-55 -50 -45

Asn Leu Leu Val Val Phe Ala Leu Thr Asn Ser Lys Lys Pro Lys Ser  
-40 -35 -30

Val Thr Asp Ile Tyr Leu Leu Asn Leu Ala Leu Ser Asp Leu Leu Phe  
-25 -20 -15

Val Ala Thr Leu Pro Phe Trp Thr His Tyr Leu Ile Asn Glu Lys Gly  
-10 -5 1 5

Leu His Asn Ala Met Cys  
10

